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- ☐ 1. [20050227248](#). 08 Oct 04. 13 Oct 05. Polypeptides having beta-1,4-GalNAc transferase activity. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/471 435/69.1 435/85 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/28 C12N009/10 C12N015/74 C12N001/21.
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- ☐ 2. [20050084891](#). 08 Oct 04. 21 Apr 05. Beta 1,4-N-acetylgalactosaminyl transferases from *C. jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 514/54 536/23.2 536/53 C12Q001/68 A61K031/739 C07H021/04 C08B037/00 C12N009/10 C12N015/74.
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- ☐ 3. [20050064550](#). 22 Apr 04. 24 Mar 05. Nucleic acids encoding beta 1,4-N-acetylgalactosaminyltransferases from *C. Jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.33 435/320.1 536/23.2 536/53 C12N009/10 C12N001/21 C12N015/74.
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- ☐ 4. [20050048630](#). 08 Oct 04. 03 Mar 05. Nucleic acids encoding beta 1,4-N-acetylgalactosaminyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/85; 435/193 435/252.3 435/320.1 435/69.1 514/54 536/23.2 536/53 C07H021/04 C08B037/00 A61K031/739 C12P019/28 C12N009/10 C12N015/74.
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- ☐ 5. [20040265875](#). 24 Apr 04. 30 Dec 04. Beta 1,4-N-acetylgalactosaminyltransferases form *C. jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12Q001/68 C07H021/04 C12N009/10 C08B037/00 C12N015/74.
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- ☐ 6. [20040259203](#). 19 May 04. 23 Dec 04. Nucleic acids encoding beta 1,3-galactosyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 514/54 536/23.2 536/53 C08B037/00 C07H021/04 C12N009/10.
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- ☐ 7. [20040259140](#). 21 May 04. 23 Dec 04. Beta 1,3-galactosyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/18 C08B037/00 C12N009/10.
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- ☐ 8. [20040229313](#). 08 Apr 04. 18 Nov 04. Sialyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.33 435/320.1 514/54 536/23.2 536/54 A61K031/739 C07H021/04 C12N009/10 C12N001/21 C12N015/74.
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- ☐ 9. [20040229272](#). 17 May 04. 18 Nov 04. Beta 1,3-galactosyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 435/89 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/30 C12N009/10 C12N015/74.
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- ☐ 10. [20040229263](#). 08 Apr 04. 18 Nov 04. Los locus from *C.jejuni*. Gilbert, Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 435/89 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/30 C12N009/10 C12N015/74.
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- ☐ 11. [20040219638](#). 14 May 04. 04 Nov 04. Nucleic acids encoding beta 1,3-galactosyltransferases from *C.jejuni*. Gilbert, Michel, et al. 435/69.3; 435/193 435/252.3 435/320.1 514/54 536/23.2 536/53 C07H021/04 A61K031/715 C08B037/00 C12N009/10.
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- ☐ 12. [20040203113](#). 12 May 04. 14 Oct 04. Nucleic acids encoding beta 1,4-N-

acetylglactosaminyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/320.1 435/325 536/23.2 536/53 C12P019/18 C07H021/04 C12N009/10 C08B037/00.

☐ 13. 20040203112. 12 May 04. 14 Oct 04. Beta1,4-N-acetylglactosaminyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/320.1 435/325 536/23.2 536/53 C12P019/18 C07H021/04 C08B037/00 C12N009/10.

☐ 14. 20040203103. 07 Apr 04. 14 Oct 04. Nucleic acids encoding sialyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 435/325 536/23.2 C12N009/10 C07H021/04 C12N001/21.

☐ 15. 20040180406. 11 Dec 03. 16 Sep 04. Nucleic acids encoding sialyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/200 435/252.3 435/320.1 536/23.2 536/53 C12N009/10 C07H021/04 C08B037/00 C12N001/21 C12N015/74.

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☐ 17. 20030186414. 11 Dec 02. 02 Oct 03. Nucleic acid that encodes a fusion protein. Gilbert, Michel, et al. 435/193; 435/320.1 435/325 435/6 435/69.1 536/23.2 C12N009/10 C12Q001/68 C07H021/04 C12P021/02 C12N005/06.

☐ 18. 20030180928. 11 Dec 02. 25 Sep 03. Fusion protein comprising a UDP-Galnac 4' epimerase and a galnac transferase. Gilbert, Michel, et al. 435/193; 435/320.1 435/325 435/6 435/69.7 536/23.2 C12N009/10 C12Q001/68 C07H021/04 C12P021/04 C12N005/06.

☐ 19. 20030157658. 21 Nov 02. 21 Aug 03. Polypeptides having beta-1,4-GalNAc transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.33 435/320.1 435/69.1 536/23.2 536/53 C12P021/02 C12N001/21 C07H021/04 C08B037/00 C12P019/26 C12N009/10 C12N015/74.

☐ 20. 20030157657. 21 Nov 02. 21 Aug 03. Polypeptides having beta-1,3-galactosyl transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C07H021/04 C08B037/00 C12N009/10 C12P021/02 C12N001/21 C12N015/74.

☐ 21. 20030157656. 21 Nov 02. 21 Aug 03. Nucleic acids encoding beta-1,4-GalNAc transferase. Gilbert, Michel, et al. 435/84; 435/193 435/252.33 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C08B037/00 C12N009/10 C07H021/04 C12P021/02 C12N001/21 C12N015/74.

☐ 22. 20030157655. 21 Nov 02. 21 Aug 03. Nucleic acids encoding polypeptides with beta-1,3-galactosyl transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C12P021/02 C12N001/21 C07H021/04 C08B037/00 C12N009/10 C12N015/74.

☐ 23. 20030148459. 21 Nov 02. 07 Aug 03. Polypeptides having sialyltransferase activity. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 536/23.2 536/53 C12P021/02 C12N001/21 C07H021/04 C12N009/10.

☐ 24. 20030049270. 29 Jan 02. 13 Mar 03. Lipopolysaccharide alpha-2,3 sialyltransferase of *Campylobacter jejuni* and its uses. Gilbert, Michel, et al. 424/190.1; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 A61K039/02 C07H021/04 C12P021/02 C12N001/21 C08B037/00

C12N009/10 C12N015/74.

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- ☐ 25. [20020042369](#). 21 Mar 01. 11 Apr 02. Campylobacter glycosyltransferases for biosynthesis of gangliosides and ganglioside mimics. [Gilbert](#), Michel, et al. 514/12; 435/193 435/320.1 435/325 536/23.2 A61K038/17 C07H021/04 C12N009/10.
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- ☐ 26. [20020034805](#). 14 Dec 98. 21 Mar 02. FUSION PROTEINS FOR USE IN ENZYMATIC SYNTHESIS OF OLIGOSACCHARIDES. [GILBERT](#), MICHEL, et al. 435/193; 435/183 435/200 435/320.1 435/325 536/23.2 C12N009/00.
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- ☐ 27. [6911337](#). 21 Nov 02; 28 Jun 05. Nucleic acids encoding .beta.-1,4-GalNAc transferase. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/320.1 435/325 536/23.2. C07H021/04 C12N009/10 C12N015/00 C12N001/20.
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- ☐ 29. [6825019](#). 21 Nov 02; 30 Nov 04. Polypeptides having .beta.-1,3-galactosyl transferase activity. [Gilbert](#); Michel, et al. 435/193; 435/252.3 435/252.33. C12N009/10 C12N001/20.
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- ☐ 30. [6723545](#). 21 Nov 02; 20 Apr 04. Polypeptides having .beta.-1,4-GalNAc transferase activity. [Gilbert](#); Michel, et al. 435/193;. C12N009/10.
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- ☐ 32. [6699705](#). 21 Mar 01; 02 Mar 04. Campylobacter glycosyltransferases for biosynthesis of gangliosides and ganglioside mimics. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/320.1 435/325 536/23.2. C07H021/04 C12N001/20 C12N015/63 C12N009/10.
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- ☐ 33. [6689604](#). 18 Mar 99; 10 Feb 04. Lipopolysaccharide .alpha.-2,3 sialyltransferase of Campylobacter jejuni and its uses. [Gilbert](#); Michel, et al. 435/320.1; 435/252.3 435/252.33 435/346 435/6 435/68.1 435/69.1 435/69.3 435/70.2 435/71.1 435/71.2 435/74 435/822 514/54 536/23.1 536/23.2 536/24.3. C12N015/00.
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- ☐ 34. [6503744](#). 31 Jan 00; 07 Jan 03. Campylobacter glycosyltransferases for biosynthesis of gangliosides and ganglioside mimics. [Gilbert](#); Michel, et al. 435/193; 435/183 435/252.3 435/320.1 536/23.2. C12N009/10 C12N009/00 C12N001/20 C12N015/00.
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- ☐ 37. [WO 200274942A](#). New glycosyltransferases from Campylobacter, useful for synthesizing gangliosides and ganglioside mimetics, and in studying the pathogenesis mechanisms of organisms that synthesize ganglioside mimetics. [GILBERT](#), M, et al. C07H021/04 C12N001/20 C12N005/10

C12N009/00 C12N009/10 C12N009/12 C12N015/09 C12N015/54 C12N015/63 C12Q001/68.

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☐ 39. [WO 9949051A](#). New sialyltransferases useful for adding sialyl residues to acceptor molecules. GILBERT, M, et al. A61K039/02 C07H021/04 C08B037/00 C12N001/21 C12N005/10 C12N009/10 C12N015/00 C12N015/09 C12N015/54 C12N015/70 C12N015/74 C12N015/79 C12P019/26 C12P021/02 C12Q001/48 E21B034/10.

☐ 40. [US 6096529A](#). Nucleic acid sequence encoding Neisseria alpha-2,3-sialyl:transferase - useful to add sialic acid to acceptor with terminal galactose residue for synthesis of biologically active oligosaccharide. GILBERT, M, et al. C12N001/15 C12N001/19 C12N001/21 C12N005/10 C12N009/10 C12N015/09 C12N015/54 C12N015/70 C12N015/79 C12P019/18 C12P019/26 C12N009/10 C12N015/09 C12R001:36 C12R001:36.

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Search for

ENZYME: 2.4.99.-

Release 38, September 2005, and updates up to 06-Dec-2005

Transferases

Glycosyltransferases


Transferring other glycosyl groups

All Swiss-Prot entries corresponding to class 2.4.99.-.

The following ENZYME entries belong to class 2.4.99.-:

- [2.4.99.1](#) Beta-galactoside alpha-2,6-sialyltransferase.
- [2.4.99.2](#) Monosialoganglioside sialyltransferase.
- [2.4.99.3](#) Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase.
- [2.4.99.4](#) Beta-galactoside alpha-2,3-sialyltransferase.
- [2.4.99.5](#) Galactosyldiacylglycerol alpha-2,3-sialyltransferase.
- [2.4.99.6](#) N-acetyllactosaminide alpha-2,3-sialyltransferase.
- [2.4.99.7](#) (Alpha-N-acetylneuraminy-2,3-beta-galactosyl-1,3)-N-acetyl-galactosaminide 6-alpha-sialyltransferase.
- [2.4.99.8](#) Alpha-N-acetylneuraminate alpha-2,8-sialyltransferase.
- [2.4.99.9](#) Lactosylceramide alpha-2,3-sialyltransferase.
- [2.4.99.10](#) Neolactotetraosylceramide alpha-2,3-sialyltransferase.
- [2.4.99.11](#) Lactosylceramide alpha-2,6-N-sialyltransferase.

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SEQUENCE LISTING

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Wakarchuk, Warren W.
National Research Council of Canada

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 Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn
 260 265 270
 Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu
 275 280 285
 His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val
 290 295 300
 Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His
 305 310 315 320
 Leu Ser Tyr Lys Leu Gly Gln Ala Leu Ile Ile Asn Ser Lys Ser Val
 325 330 335
 Leu Gly Phe Leu Ser Leu Pro Phe Ile Ile Leu Ser Ile Val Ile Ser
 340 345 350
 His Lys Gln Glu Gln Lys Ala Tyr Lys Phe Lys Val Lys Lys Asn Pro
 355 360 365
 Asn Leu Ala Leu Pro Pro Leu Glu Thr Tyr Pro Asp Tyr Asn Glu Ala
 370 375 380
 Leu Lys Glu Lys Glu Cys Phe Thr Tyr Lys Leu Gly Glu Glu Phe Ile
 385 390 395 400
 Lys Ala Gly Lys Asn Trp Tyr Gly Glu Gly Tyr Ile Lys Phe Ile Phe
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 Lys Asp Val Pro Arg Leu Lys Arg Glu Phe Glu Lys Gly Glu
 420 425 430

<210> 3

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ18F 5' primer

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.41

<210> 4
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CJ40R 3' primer

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<210> 5
<211> 231
<212> PRT
<213> Haemophilus influenzae

<220>
<223> Haemophilus influenzae Rd putative open reading
frame (ORF)

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1 5 10 15
Ser Ser Phe Val Asn Leu Gly Asp Ser Glu Leu Lys Lys Ile Lys Asn
20 25 30
Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn
35 40 45
Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu
50 55 60
Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val
65 70 75 80
Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu
85 90 95
Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys
100 105 110
Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser
115 120 125
Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly
130 135 140
Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe
145 150 155 160
Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys
165 170 175
Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys
180 185 190

Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe
 195 200 205

Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala
 210 215 220

Leu Lys Ser Arg Lys Trp Asp
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<210> 6

<211> 6

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:6 His tail
 (His)6

<400> 6

His His His His His His
 1 5

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<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:linker between
 two fusion protein domains

<400> 7

Gly Gly Gly His
 1



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Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: campylobacter sialyltransferase

UniProtKB/Swiss-Prot Release 48.6 of 06-Dec-2005
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-
- Number of sequences found in UniProt Knowledgebase (Swiss-Prot₍₀₎ and TrEMBL) (15): **15**
 - Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
 - For more directed searches, you can use the Sequence Retrieval System SRS.
-

Search in UniProtKB/Swiss-Prot: There are matches to 0 out of 201594 entries

Search in UniProtKB/TrEMBL: There are matches to 15 out of 2484574 entries

Q32VR8_CAMJE

Alpha-2,3-sialyltransferase {GENE:Name=cstI} - Campylobacter jejuni subsp. jejuni

Q4HEJ9_CAMCO

Alpha-2,3-sialyltransferase {GENE:ORFNames=CCO1538} - Campylobacter coli RM2228

Q4HEK5_CAMCO

Alpha-2,3-sialyltransferase {GENE:ORFNames=CCO1544} - Campylobacter coli RM2228

Q4HEL4_CAMCO

Alpha-2,3-sialyltransferase {GENE:ORFNames=CCO1527} - Campylobacter coli RM2228

Q4HGT1_CAMCO

Bifunctional alpha-2,3/-2,8-sialyltransferase {GENE:ORFNames=CCO1215} - Campylobacter coli RM2228

Q5DT12_CAMJE

Putative alpha-2,3/-2,8 sialyltransferase - Campylobacter jejuni
Q7BP25_CAMJE
Hypothetical protein Cj1140 (2,3-sialyl transferase) (Alpha-2,3-sialyltransferase)
{GENE:Name=cstIII; Synonyms=cst-III; OrderedLocusNames=Cj1140} -
Campylobacter jejuni
Q938X6_CAMJE
Alpha-2,3-/alpha-2,8-sialyltransferase {GENE:Name=cstII} - Campylobacter jejuni
Q93CZ5_CAMJE
Bifunctional alpha-2,3/-2,8-sialyltransferase {GENE:Name=cst-II} - Campylobacter
jejuni
Q93D05_CAMJE
Alpha-2,3-sialyltransferase {GENE:Name=cst-II} - Campylobacter jejuni
Q93MQ0_CAMJE
Alpha-2,3-/alpha-2,8-sialyltransferase {GENE:Name=cstII} - Campylobacter jejuni
Q9F0M9_CAMJE
Alpha-2,3-sialyltransferase {GENE:Name=cst-II} - Campylobacter jejuni
Q9L9Q5_CAMJE
Alpha-2,3-sialyltransferase {GENE:Name=cst-II; Synonyms=cst, cstII} -
Campylobacter jejuni
Q9LAK3_CAMJE
Alpha-2,3/8-sialyltransferase (Alpha-2,3/-2,8-sialyltransferase) {GENE:Name=cst-II}
- Campylobacter jejuni
Q9RGF1_CAMJE
Alpha-2,3-sialyltransferase {GENE:Name=cst-I} - Campylobacter jejuni

in Swiss-Prot/TrEMBL by AC, ID, description,
gene name, organism
**Please do NOT use any boolean operators
(and, or, etc.)**

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directory outgoing of the ExpASY anonymous ftp server, from where you can download
it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: ☒ Swiss-Prot ☐ Fasta

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If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 22 AA

Date run: 2005-12-15 23:01:28 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,699,091 sequences; 880,353,591 total letters

UniProt Knowledgebase Release 6.6 consists of:

UniProtKB/Swiss-Prot Release 48.6 of 06-Dec-2005: 201594 entries

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Db	AC	Description
----	----	-------------

<input type="checkbox"/>	sp P72074	LST_NEIGO CMP-N-acetylneuraminate-beta-galactosamide-a.
--------------------------	-----------	---

<input type="checkbox"/>	tr Q5F7T9	_NEIG1 Alpha-2,3-sialyltransferase [NGO1081] [Neisseria
--------------------------	-----------	---

CLUSTAL FORMAT for T-COFFEE Version 1.37, CPU=0.00 sec, SCORE=6070, Nseq=2, Len=431

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unk|VIRT7553|Blast_submission      MTRTRMENELIVSKNQNI IAGNGPSLKINIKRLPREYDVFRCNQFYFEDK  
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                                     *.....*.* ** ..*****
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****:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
```

```
unk|VIRT7553|Blast_submission YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEG
tr|Q93MQ0|Q93MQ0_CAMJE YDFFKQLKEFNAYFKFHEIYLNQRITSGVYMCAVAIALGYKEIYLSGIDFYQN
*:.:.:***** *:.:.:*****:*****:***** *:.:*****:.
```

```
unk|VIRT7553|Blast_submission AMSTNIKTIFPGIKDFKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSLA
tr|Q93MQ0|Q93MQ0_CAMJE TKQENLLKLAPDFKNDRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLA
: . *: : : *::: : : ***: *:***::: : *: : * ** : :***
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```
unk|VIRT7553|Blast_submission      NINNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKD
tr|Q93MQ0|Q93MQ0_CAMJE             NLNSNFIIQEK-NNYTKDILIPSSEAYGKFSKN-----INF-----
*:***:***:****:***                      ***
```

```
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                                     : *  ** : *** : : : :
```

```
unk|VIRT7553|Blast_submission      PRLKREFEKGGE
tr|Q93MQ0|Q93MQ0_CAMJE             PSDIKHYFKGK
                                     *   :   **:
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CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.00 sec, SCORE=6070, Nseq=2, Len=431

```

unk|VIRT7553|Blast_submission  MTRTRMENELIVSKNMQNIIAGNGPSLKNINYNKRLPREYDVFRCNQFYFEDK
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                                *:::*:*****:*.****:;*****
                                *

unk|VIRT7553|Blast_submission  KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNF
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                                ****:***:*.::*: *:* *::*** : *:*.* ..*.:*: *::
                                *

unk|VIRT7553|Blast_submission  YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEG
tr|Q93MQ0|Q93MQ0_CAMJE        YDFFKQLKEFNAYFKFHEIYLNQRITSGVYMCAVAIALGYKEIYLSGIDFYQN
                                *:..:***** **.*:*****:*****:***** **.******;.
                                *

unk|VIRT7553|Blast_submission  AMSTNIKTIFPGIKDFKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSIILA
tr|Q93MQ0|Q93MQ0_CAMJE        TKQENLLKLAPDFKNDRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLA
                                : . *: .: *.:*: :.      ***: **:*::*:.. **::*.** :*:**
                                *

unk|VIRT7553|Blast_submission  NINNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKD
tr|Q93MQ0|Q93MQ0_CAMJE        NLNSNFIIQEK-NNYTKDILIPSSEAYGKFSKN-----INF-----
                                *:*.* ** :*: * ** :***:.. . . * **      :**
                                *

unk|VIRT7553|Blast_submission  KEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSKSVLGFSLPFIILSIVIS
tr|Q93MQ0|Q93MQ0_CAMJE        -----
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unk|VIRT7553|Blast_submission  YKFKVKKNPNLALPPLETYPDYNEALKEKECFYKLGEEFIKAGKNWYGEgyI
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                                : : * ** : *** ::::
                                *

unk|VIRT7553|Blast_submission  PRLKREFEKGE
tr|Q93MQ0|Q93MQ0_CAMJE        PSDIKHYFKGK
                                *   :.: **;
                                *

```

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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query: 430 AA

Date run: 2005-12-15 16:31:23 UTC+0100 on sib-gm1.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,699,091 sequences; 880,353,591 total letters

UniProt Knowledgebase Release 6.6 consists of:

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List of potentially matching sequences

Send selected sequences to

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Db	AC	Description
----	----	-------------

- | | | |
|--------------------------|-----------|--|
| <input type="checkbox"/> | tr Q32VR8 | _CAMJE Alpha-2,3-sialyltransferase [cstI] [Campylobacter] |
| <input type="checkbox"/> | tr Q9RGF1 | _CAMJE Alpha-2,3-sialyltransferase [cst-I] [Campylobacter] |

☐ tr Q5DT12 _CAMJE Putative alpha-2,3/-2,8 sialyltransferase [Campy
☐ tr Q93MQ0 _CAMJE Alpha-2,3-/alpha-2,8-sialyltransferase [cstII] [
☐ tr Q9F0M9 _CAMJE Alpha-2,3-sialyltransferase [cst-II] [Campylobac
☐ tr Q9LAK3 _CAMJE Alpha-2,3/8-sialyltransferase (Alpha-2,3-/2,8-si
☐ tr Q9L9Q5 _CAMJE Alpha-2,3-sialyltransferase [cst-II] [Campylobac
☐ tr Q938X6 _CAMJE Alpha-2,3-/alpha-2,8-sialyltransferase [cstII] [
☐ tr Q50FZ0 _CAMJE Cj81-011 (Fragment) [Campylobacter jejuni]
☐ tr Q93CZ5 _CAMJE Bifunctional alpha-2,3/-2,8-sialyltransferase [c
☐ tr Q93D05 _CAMJE Alpha-2,3-sialyltransferase [cst-II] [Campylobac
☐ tr Q7BP25 _CAMJE Hypothetical protein Cj1140 (2,3-sialyl transfer
☐ tr Q32VQ2 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q4QM36 _HAEI8 CMP-neu5Ac--lipooligosaccharide alpha 2-3 sialyl
☐ tr Q32VR2 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q5W602 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q5M6Q2 _CAMJE Putative sugar transferase [HS23.17] [Campylobac
☐ tr Q9CLP3 _PASMU Hypothetical protein PM1174 [PM1174] [Pasteurell
☐ tr Q6EF79 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q4QNI8 _HAEI8 CMP-Neu5Ac--lipooligosaccharide alpha 2-3 sialyl
☐ tr Q6EF56 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q5W603 _CAMJE Hypothetical protein [Campylobacter jejuni]
☐ tr Q32VQ8 _CAMJE Hypothetical protein [Campylobacter jejuni subsp
☐ tr Q32VR3 _CAMJE Hypothetical protein [Campylobacter jejuni subsp
☐ tr Q32VQ3 _CAMJE Hypothetical protein [Campylobacter jejuni subsp
☐ tr Q5HT01 _CAMJR Capsular polysaccharide biosynthesis protein, pu
☐ tr Q5M6U5 _CAMJE Putative sugar transferase [HS41.06] [Campylobac
☐ tr Q6EBB5 _CAMJE Tgh007 (Fragment) [Campylobacter jejuni]
☐ tr Q4HEK5 _CAMCO Alpha-2,3-sialyltransferase [CC01544] [Campyloba
☐ tr Q4HEL4 _CAMCO Alpha-2,3-sialyltransferase [CC01527] [Campyloba
☐ tr Q4HEJ9 _CAMCO Alpha-2,3-sialyltransferase [CC01538] [Campyloba
☐ sp P24324 Y352_HAEIN Hypothetical protein HI0352 (ORF1) [HI0352].
☐ tr Q5M6M2 _CAMJE Putative sugar transferase [HS19.11] [Campylobac
☐ tr Q5M6M5 _CAMJE Putative sugar transferase [HS19.08] [Campylobac
☐ tr Q5HT02 _CAMJR Capsular polysaccharide biosynthesis protein, pu
☐ tr Q4HR89 _CAMUP Hypothetical protein [CUP1274] [Campylobacter up
☐ tr Q4HEL1 _CAMCO DcbE, putative [CC01537] [Campylobacter coli RM2
☐ tr Q9PMM6 _CAMJE Hypothetical protein Cj1431c [Cj1431c] [Campylob
☐ tr Q50FV9 _CAMJE Cj81-063 (Fragment) [Campylobacter jejuni]
☐ tr Q4HR98 _CAMUP Hypothetical protein [CUP1265] [Campylobacter up
☐ tr Q4HKU2 _CAMLA Glycosyl transferase family 8 family [CLA1010] [
☐ tr Q5M6U6 _CAMJE Putative sugar transferase [HS41.05] [Campylobac
☐ tr Q5M6S8 _CAMJE Putative sugar transferase [HS41.23] [Campylobac
☐ tr Q6EF57 _CAMJE Putative glycosyltransferase (Putative sugar tra

☐ tr Q4HR96 _CAMUP Glycosyl transferase, group 2 family protein [CU
☐ tr Q4HLH9 _CAMLA Hypothetical protein [CLA0678] [Campylobacter la
☐ tr Q9PMN6 _CAMJE Possible sugar transferase [Cj1421c] [Campylobac
☐ tr Q9PMN5 _CAMJE Possible sugar transferase [Cj1422c] [Campylobac
☐ tr Q6EF89 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q6EF76 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q5M6M6 _CAMJE Putative sugar transferase [HS19.07] [Campylobac
☐ tr Q9PMM3 _CAMJE Putative sugar transferase [Cj1434c] [Campylobac
☐ tr Q4HR95 _CAMUP Glycosyl transferase, group 2 family protein, pu
☐ tr Q5M6R2 _CAMJE Putative sugar transferase [HS23.07] [Campylobac
☐ tr Q5M6P9 _CAMJE Putative sugar transferase (Cj81-080) [HS23.20]
☐ tr Q4HRA0 _CAMUP Glycosyl transferase family 8 family [CUP1263] [
☐ tr Q4HSD1 _CAMUP Probable sugar transferase Cj1422c [CUP0322] [Ca
☐ tr Q4HQ44 _CAMUP Probable sugar transferase Cj1422c [CUP1233] [Ca
☐ tr Q4HLH0 _CAMLA Probable sugar transferase Cj1422c [CLA0667] [Ca
☐ tr Q4HLF9 _CAMLA Probable sugar transferase Cj1421c [CLA0655] [Ca
☐ tr Q4HNW9 _CAMUP Capsular polysaccharide biosynthesis protein, pu
☐ tr Q9PML9 _CAMJE Putative sugar transferase [Cj1438c] [Campylobac
☐ tr Q4HQ73 _CAMUP Capsular polysaccharide biosynthesis protein, pu
☐ tr Q9PMM5 _CAMJE Putative sugar transferase [Cj1432c] [Campylobac
☐ tr Q4HTL3 _CAMUP Hypothetical protein [CUP0667] [Campylobacter up
☐ tr Q5M6N9 _CAMJE Putative sugar transferase [HS1.07] [Campylobact
☐ tr Q50FW8 _CAMJE Cj81-047 (Fragment) [Campylobacter jejuni]
☐ tr Q5M6S9 _CAMJE Putative sugar transferase [HS41.22] [Campylobac
☐ tr Q9CMP1 _PASMU HyaE (FcbE) [hyaE] [Pasteurella multocida]
☐ tr Q4HGT1 _CAMCO Bifunctional alpha-2,3/-2,8-sialyltransferase [C
☐ tr O85456 _PASMU HyaE [hyaE] [Pasteurella multocida]
☐ tr Q4HS04 _CAMUP Hypothetical protein [CUP1761] [Campylobacter up
☐ tr Q9AHN3 _PASMU DcbE [dcbE] [Pasteurella multocida]
☐ tr Q8L0V3 _ECOLI Hypothetical protein kfoB [kfoB] [Escherichia co.
☐ tr Q6EBB2 _CAMJE Tgh012 (Fragment) [Campylobacter jejuni]
☐ tr Q4HTC3 _CAMUP Capsular polysaccharide biosynthesis protein, pu
☐ tr Q6KCZ4 _ECOLI KfiB protein [kfiB] [Escherichia coli]
☐ tr Q43KB3 _9CHLB Similar to Chromosome segregation ATPases [Cpha2
☐ tr Q6EBB6 _CAMJE Tgh006 (Fragment) [Campylobacter jejuni]
☐ tr Q6EB08 _CAMJE Tgh120 (Fragment) [Campylobacter jejuni]
☐ tr Q8IBW2 _PLAF7 Hypothetical protein MAL7P1.65 [MAL7P1.65] [Plas
☐ tr Q4Y918 _PLACH Hypothetical protein (Fragment) [PC000047.00.0]
☐ tr Q4HTQ9 _CAMUP Hypothetical protein [CUP0614] [Campylobacter up
☐ tr Q9EMR1 _AMEPV AMV138 [AMV138] [Amsacta moorei entomopoxvirus (
☐ tr Q7RS84 _PLAYO TERT (Fragment) [PY00479] [Plasmodium yoelii yoe
☐ tr Q8I474 _PLAF7 Hypothetical protein PFE0130c [PFE0130c] [Plasmo

☐ tr Q8I3Z1 _PLAF7 Hypothetical protein PFE0570w [PFE0570w] [Plasmo
☐ tr Q55FU8 _DICDI Hypothetical protein [DDB0189664] [Dictyostelium
☐ tr Q7RCB6 _PLAYO Hypothetical protein [PY05868] [Plasmodium yoeli
☐ tr Q8ILS2 _PLAF7 Hypothetical protein [PF14_0172] [Plasmodium fal
☐ tr Q4YMV9 _PLABE Hypothetical protein (Fragment) [PB001093.03.0]
☐ tr Q6EF78 _CAMJE Putative glycosyltransferase (Putative sugar tra
☐ tr Q6EF55 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q98RL8 _GUITH Hypothetical protein orf714 [orf714] [Guillardia
☐ tr Q7QPQ2 _GIALA GLP_348_13351_18885 [Giardia lamblia ATCC 50803]
☐ tr P73984 _SYNY3 Slr2117 protein [slr2117] [Synechocystis sp. (st
☐ tr Q5M6S3 _CAMJE Putative sugar transferase [HS41.28] [Campylobac
☐ tr Q8EWI3 _MYCPE Hypothetical protein MYPE2220 [MYPE2220] [Mycopl
☐ tr Q8I232 _PLAF7 Hypothetical protein PFA0550w [PFA0550w] [Plasmo
☐ tr Q8IDZ6 _PLAF7 Hypothetical protein PF13_0182 [PF13_0182] [Plas

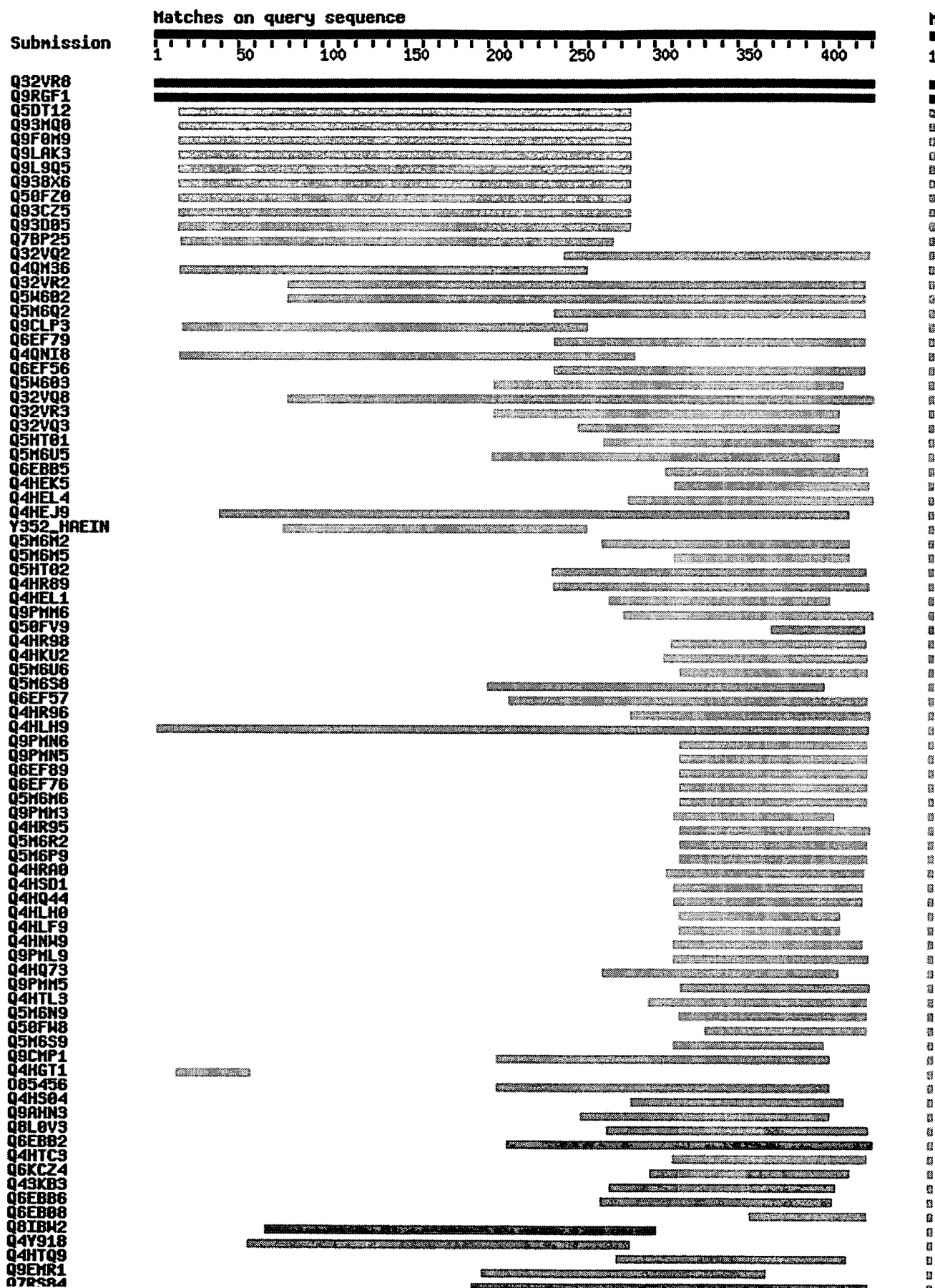
Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE
profiles or Pfam HMMs
([?](#) Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

CST-I



Alignments

tr Q32VR8 Alpha-2,3-sialyltransferase [cstI] [Campylobacter
Q32VR8_CAMJE jejuni subsp.
jejuni]

Score = 877 bits (2266), Expect = 0.0

Identities = 430/430 (100%), Positives = 430/430 (100%)

Query: 1 MTRTRMENELIVSKNMQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYLL
MTRTRMENELIVSKNMQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYLL
Sbjct: 1 MTRTRMENELIVSKNMQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYLL

Query: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNFFPD
KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNFFPD
Sbjct: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNFFPD

Query: 121 YEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
YEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
Sbjct: 121 YEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI

Query: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFP
AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFP
Sbjct: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFP

Query: 241 INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKDTLIK
INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKDTLIK
Sbjct: 241 INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKDTLIK

Query: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE
EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE
Sbjct: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE

Query: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIF
KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIF
Sbjct: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIF

Query: 421 RLKREFEKGE 430
RLKREFEKGE
Sbjct: 421 RLKREFEKGE 430

tr Q9RGF1 Alpha-2,3-sialyltransferase [cst-I] [Campylobacter
Q9RGF1_CAMJE jejuni]

Score = 875 bits (2261), Expect = 0.0

Identities = 429/430 (99%), Positives = 429/430 (99%)

```
Query: 1  MTRTRMENELIVSKNMQNI IIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYL
          MTRTRMENELIVSKNMQNI IIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYL
Sbjct: 1  MTRTRMENELIVSKNMQNI IIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYL

Query: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPD
          KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPD
Sbjct: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPD

Query: 121 YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
          YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
Sbjct: 121 YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI

Query: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP
          AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP
Sbjct: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP

Query: 241 INNNFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFYNI LHSKDTLIK
          INNNFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFYNI LHSKDTLIK
Sbjct: 241 INNNFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFYNI LHSKDTLIK

Query: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE
          EIAVLKKQTTQRAKARIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE
Sbjct: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE

Query: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE GYIKFIF
          KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE GYIKFIF
Sbjct: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE GYIKFIF

Query: 421 RLKREFEKGE 430
          RLKREFEKGE
Sbjct: 421 RLKREFEKGE 430
```

```
tr  Q5DT12          Putative alpha-2,3/-2,8 sialyltransferase
    Q5DT12_CAMJE    [Campylobacter jejuni]
```

Score = 301 bits (770), Expect = 3e-80

Identities = 147/274 (53%), Positives = 189/274 (68%), Gaps = 7/27

```
Query: 16  MQNI IIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYLGKKIKAVFFNPGVFL
          M+ +IIAGNGPSLK I+Y RLP ++DVFR CNQFYFEDKYYLGKK KAVF+NP +F
Sbjct: 1  MKKVIIAGNGPSLKEIDYSRLPNDFDVFR CNQFYFEDKYYLGKKCKAVFYNP SLFF

Query: 76  TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPD AKLGYEV IENLKEFY
```



```

      T K LI   EYE + I CS FNL   IES +FL  FY++FPDA LGY+   + LKEF
Sbjct: 61  TLKHLIQNQEYETELIVCSNFNLTTHIESENFLKNFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
      ++EIYFN+RITSG+YMCA+AIALGYK IYL GIDFY+   Y F+   N+   +
Sbjct: 121 FHEIYFNQRITSGIYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQKNLLKL--

Query: 196 FKPSNC---HSKEYDIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTL
      FK N      HSK  D++AL+ L+  YK+ +Y LC +S+LAN  L+ N+N+NF +
Sbjct: 178 FKNDNSHYIGHSKNTDLKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFII

Query: 252 NNSINDILLTDNTPGVSFYKNQLKADNKIMLNIFY 285
      NN  DIL+  +      F KN +      KI  N Y
Sbjct: 238 NNYTKDILIPSSEAYGKFSKNIIFKKIKIKENIY 271

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tr   Q93MQ0                Alpha-2,3-/alpha-2,8-sialyltransferase [cstII]
      Q93MQ0_CAMJE          [Campylobacter
                          jejuni]

```

Score = 290 bits (742), Expect = 6e-77

Identities = 142/271 (52%), Positives = 186/271 (68%), Gaps = 2/27

```

Query: 16  MQNIIIIAGNGPSLKNINYNKRLPREYDVFRCNQFYFEDKYYLGKKIKAVFFNPGVFL
      M+ +II+GNGPSLK I+Y RLP ++DVFRCNQFYFEDKYYLGKK KAVF+NPG+F
Sbjct: 1   MKKVIIISGNGPSLKEIDYSRLPNDFDVFRCNQFYFEDKYYLGKKFKAVFYNPGLFF

Query: 76  TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENTLKEFY
      T K LI   EYE + I CS +N   +E+ +F+  FY++FPDA LGY+   + LKEF
Sbjct: 61  TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
      ++EIY N+RITSGVYMCA+AIALGYK IYL GIDFY+   Y F+   N+   + P
Sbjct: 121 FHEIYLNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTLENK
      +      HSK  DI+AL+ L+  YK+ +Y LC +S+LAN  L+ N+N+NF ++ K
Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNIFY 285
      DIL+  +      F KN      KI  N Y
Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENIY 270

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tr   Q9F0M9                Alpha-2,3-sialyltransferase [cst-II] [Campylobacter

```

Q9F0M9_CAMJE jejuni]

Score = 290 bits (741), Expect = 8e-77

Identities = 143/271 (52%), Positives = 185/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYYLGKKIKAVFFNPGVFL
M+ +IIAGNGPSLK I+Y RLP ++DVFRNCFYFEDKYYLGKK KAVF+ PG F
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCFYFEDKYYLGKKCKAVFYTPGFFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDALGYEVIENLKEFY
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P
Sbjct: 121 FHEIYFNQRITSGVYMCAVAIAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K
Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
DIL+ + F KN KI N Y
Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENVY 270

tr Q9LAK3 Alpha-2,3/8-sialyltransferase (Alpha-2,3-/2,8-
Q9LAK3_CAMJE sialyltransferase)
 [cst-II] [Campylobacter jejuni]

Score = 288 bits (736), Expect = 3e-76

Identities = 143/271 (52%), Positives = 185/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYYLGKKIKAVFFNPGVFL
M+ +IIAGNGPSLK I+Y RLP ++DVFRNCFYFEDKYYLGKK KAVF+NP +F
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCFYFEDKYYLGKKCKAVFYNPILFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDALGYEVIENLKEFY
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LK+F
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKDFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P
Sbjct: 121 FHEIYFNQRITSGVYMCAVAIAIALGYKEIYLSGIDFYQNGSSYAFDTKQKNLLKLAP

Query: 195 DFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
D HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K

Sbjct: 181 DNSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285

DIL+ + F KN KI N Y

Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENIY 270

tr Q9L9Q5 Alpha-2,3-sialyltransferase [cst-II] [Campylobacter
Q9L9Q5_CAMJE jejuni]

Score = 287 bits (735), Expect = 4e-76

Identities = 142/271 (52%), Positives = 184/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYYLGKKIKAVFFNPGVFL
M+ +IIAGNGPSLK I+Y RLP ++DVFRNCFYFEDKYYLGKK KAVF+ P F

Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCFYFEDKYYLGKKCKAVFYTPNFFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDACLGYEVIENTLKEFY
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF

Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P

Sbjct: 121 FHEIYFNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K

Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285

DIL+ + F KN KI N Y

Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENVY 270

tr Q938X6 Alpha-2,3-/alpha-2,8-sialyltransferase [cstII]
Q938X6_CAMJE [Campylobacter
jejuni]

Score = 287 bits (735), Expect = 4e-76

Identities = 142/271 (52%), Positives = 184/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYYLGKKIKAVFFNPGVFL
M+ +II+GNGPSLK I+Y RLP ++DVFRNCFYFEDKYYLGKK KAVF+NP +F

Sbjct: 1 MKKVIIISGNGPSLKEIDYSRLPNDFDVFRNCFYFEDKYYLGKKCKAVFYNP SLFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENLKEFY
T K LI EYE + I CS FN +E+ +F+ FY++FPDA LGY+ + LKEF
Sbjct: 61 TLKHLIQNQEYETELIMCSNFNQAHLENQNFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIIYFN+RITSGVYMC +AIALGYK IYL GIDFY+ Y F+ N+ + P
Sbjct: 121 FHEIYFNQRITSGVYMCTVAIALGYKEIYLSGIDFYQNGSSYAFDTKQKNLLKLAP

Query: 195 DFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
D HSK DI+AL+ L+ Y++ +Y LC +S+LAN L+ N+N+NF ++ K
Sbjct: 181 DNSHYIGHSKNTDIKALEFLEKTYEIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
DIL+ + F KN KI N Y
Sbjct: 240 TKDILIPSSEAYGKFTKNINFKKIKIKENIY 270

tr Q50FZ0 Cj81-011 (Fragment) [Campylobacter jejuni] 2
Q50FZ0_CAMJE a

Score = 287 bits (735), Expect = 4e-76

Identities = 142/271 (52%), Positives = 184/271 (67%), Gaps = 2/27

Query: 16 MQNIIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKY YLGKKIKAVFFNPGVFL
M+ +IIAGNGPSLK I+Y RLP ++DVFRCNQFYFEDKY YLGKK KAVF+ P F
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRCNQFYFEDKY YLGKKCKAVFYTPNFFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENLKEFY
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P
Sbjct: 121 FHEIYFNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K
Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
DIL+ + F KN KI N Y
Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENVY 270

tr Q93CZ5 Bifunctional alpha-2,3/-2,8-sialyltransferase [cst-

Q93CZ5_CAMJE

II]

[Campylobacter jejuni]

Score = 287 bits (734), Expect = 5e-76

Identities = 142/271 (52%), Positives = 185/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYYLGKKIKAVFFNPGVFL
M+ +II+GNGPSLK I+Y RLP ++DVFRNCFYFEDKYYLGKK KAVF+NP +F
Sbjct: 1 MKKVIIISGNGPSLKEIDYSRLPNDFDVFRNCFYFEDKYYLGKKCKAVFYNP SLFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENTLKEFY
T K LI EYEI+ I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF
Sbjct: 61 TLKHLIQNQEYEIELIMCSNYNQAHLNENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIYFN+RITSGVYMC +AIALGYK IYL GIDFY+ Y F+ N+ + P
Sbjct: 121 FHEIYFNQRITSGVYMCTVAIALGYKEIYLSGIDFYDNGGGYAFDTKQKNLLKLAP

Query: 195 DFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
D HSK DI+AL+ L+ Y++ +Y LC +S+LAN L+ N+N+NF ++ K
Sbjct: 181 DNSHYIGHSKNTDIKALEFLEKTYEIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
DIL+ + F KN KI N Y
Sbjct: 240 TKDILIPSSEAYGKFTKNINFKKIKIKENIY 270

tr Q93D05
Q93D05_CAMJE

Alpha-2,3-sialyltransferase [cst-II] [Campylobacter
jejuni]

Score = 286 bits (731), Expect = 1e-75

Identities = 141/271 (52%), Positives = 183/271 (67%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCFYFEDKYYLGKKIKAVFFNPGVFL
M+ +IIAGNGPSLK I+Y RLP ++DVFRNCFYFEDKYYLGKK K VF+ P F
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCFYFEDKYYLGKKCKTVFYTPNFFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENTLKEFY
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLNENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIYFN+RITSGVYMC+AIALGYK IYL GIDFY+ Y F+ N+ + P
Sbjct: 121 FHEIYFNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K

Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285

DIL+ + F KN KI N Y

Sbjct: 240 TKDILIPSSEAYGKFSSKNINFKKIKIKENVY 270

tr Q7BP25 Hypothetical protein Cj1140 (2,3-sialyl
Q7BP25_CAMJE transferase)
(Alpha-2,3-sialyltransferase) [cstIII]
[Campylobacter
jejuni]

Score = 261 bits (667), Expect = 3e-68

Identities = 136/263 (51%), Positives = 182/263 (68%), Gaps = 10/2

Query: 18 NIIIAGNGPSLKNINIKRLPREYDVFRNCFYFEDKYLLGKKIKAVFFNPQVFLQQ
N ++ GNGPSLKNI+YKRLP+++DVFRNCFYFED+Y++GK +K VFFNP VF +Q

Sbjct: 6 NALVCGNGPSLKNIDYKRLPKQFDVFRNCFYFEDRYFVGKDVKYVFFNPVFFFEQ

Query: 78 KQLILKNEYEIKNIFCSTFNLPIESNDFLHQFYNFPPDAKLGYEVIENTLKEFYAY
K+LI EY I+NI CST NL +I+ F+ F +F DA LG+E+I+ LK+F+AY

Sbjct: 66 KKLIQNEEYNIENIVCSTINLEYIDGFQFVDNFELYFSDAFLGHEIIKKLKDFEFAY

Query: 138 EIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEG-DVIYPFEAMSTNIKTIFPG
EIY +RITSGVYMCA A+ALGYK+IY+ GIDFY+ + +Y F+ N+ G

Sbjct: 126 EIYNRQRITSGVYMCATAVALGYKSIYISGIDFYQDTNNLYAFDNNKKNLLNKCTG

Query: 196 -FKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
FK N HS D++AL L Y VNIY+L D +F L+ +I ++F L K

Sbjct: 186 KFKFIN-HSMACDLQALDYLKRYDVNIYSLNSD----EYFKLAPDIGSDFVLSKK

Query: 255 INDILLTDNTPGVSFY--KNQLK 275

INDIL+ D +Y K++LK

Sbjct: 241 INDILIPDKYAQERYYGKKSRLK 263

tr Q32VQ2 Putative glycosyltransferase [Campylobacter jejuni
Q32VQ2_CAMJE subsp. jejuni]

Score = 229 bits (585), Expect = 9e-59

Identities = 125/206 (60%), Positives = 143/206 (68%), Gaps = 24/2

Query: 247 LENKHNNNSINDILLTDNTPGV-----SFYKNQLKADNKIMLN
+ NK+ N++ + LL D + Y ++ + K++ N

Sbjct: 327 IANKYQNTVLENLLNDRISALWQILDCKDPLDILNKIPKKLYIKKVFSLKVKIKN

Query: 288 LHSKDTLIKFLNKEIAVLKKQTT-----QRAKARIQNHLASYKLGQALIINSKSVLG
L +K T+I +I L K +AK RIQN LSYKLGQALIINSKSVLG
Sbjct: 387 LENKKTIIINQTNQIHNLNKTlnfQNNYgKAKIRIQNQLSYKLGQALIINSKSVLG

Query: 343 PFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEE
PFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEE
Sbjct: 447 PFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEE

Query: 403 GKNWYGEgyIKFIFKdVpRLKREFEK 428
KNWYG GYIKF FKdVpRLKRE+++
Sbjct: 507 SKNWYGGGYIKFYFKdVpRLKREYKR 532

tr Q4QM36 CMP-neu5Ac--lipooligosaccharide alpha 2-3
Q4QM36_HAEI8 sialyltransferase
[lic3A2] [Haemophilus influenzae (strain 86-028NP)]

Score = 222 bits (565), Expect = 2e-56
Identities = 124/248 (50%), Positives = 161/248 (64%), Gaps = 6/24

Query: 17 QNIIIAGNGPSLKNINyKRLPREYDVFRcNQFYFEDKYyLGKKIKAVFFNPGVFLQ
+++IIAGNG SLK+I+Y LP++YDVFRcNQFYFED Y+LGKKIK VFFN V +
Sbjct: 32 KSVIIAGNGTSLKSIDYSLLPKDyDVFRcNQFYFEDHYFLGKKIKKVFFNCSVIFE

Query: 77 AKQLILKNEYEIKNIFCSTF-NLPFIESNDfLHQFYNFFPDakLGYEVIENLKEFY
QLI NEYE +I S+F NL E + + P LG+ ++ L+ F
Sbjct: 92 FMQLIKNNEYEYADIILSSfLNLGDSELKK-IQRLEKLLPQIDLGHSyLKKLRAFD

Query: 136 YNEIyFNKRITSGVYMCAIAIALGYKTIyLcGIDFY-EGDVIyPFAMSTNIKTIF
Y+E+Y NKRITSGVYMCA+A A+GYK +YL GIDFY E Y F + NI +
Sbjct: 151 YHELYENKRITSGVYMCAVATAMGYKDLYLTGIDFYQEKGNPYAFHHQTENIIKLL

Query: 195 DFK-PSNCHSKEYDIEALKLLKSIyKVNIyALCDDSiLANHFPLS-ININNNFTLE
K S+ HS EYD+ AL L+ Y VNIY + +S L N+FPLS +N F LE
Sbjct: 211 QNKSQSDIHSMEYDLNAlYFLQKHYGvNIyCISPESPLCNyFPLSPLNNPITFILE

Query: 253 NSINDILL 260
+ DIL+
Sbjct: 271 YT-QDILI 277

tr Q32VR2 Putative glycosyltransferase [Campylobacter jejuni
Q32VR2_CAMJE subsp. jejuni]

Score = 219 bits (557), Expect = 2e-55

Identities = 146/357 (40%), Positives = 196/357 (54%), Gaps = 35/3

```
Query: 81  ILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYE-----VIENLKEFY
          I+  ++    + C   N  +I  N      Y   P++ + Y      + ++LK F
Sbjct: 242  IIHEDHHFGMLLCLQANKIYINLNKLY--IYRVRPNSIMNYNDNGKNINKSLKNFC

Query: 136  YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNI--KTI
          N I   K      Y      +AL +          +F+  D+I  F      N      I
Sbjct: 300  LNVIDGKKYYKILSYGINAFLALNFSN-----NFHNKDLIKLFNKAFKNECENWI

Query: 194  KDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLEN
          +  ++   S      IE  +++K+ Y+ N   L   D I          ++ INNN
Sbjct: 354  AQYPTNDLRS--LFIEIFRIMKN-YETNYENLILDFI-----AMIINNNKITIV

Query: 254  SINDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKDTLIK-----FLNKEIAV
          I +      N   + Y  ++ + N I+L   N +H+ +T ++      + KE  +
Sbjct: 404  EIQN-----NQNTIKIYCEKINSQNNIILQQTNQIHNLNTTLENKNQLLITKENLL

Query: 309  TTQRAKARIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKV
          +AK R+QN LSYKLGQALI+NSKSVLGFLSLPFIILSI+ISHKQEQKAYKFKV
Sbjct: 459  NYGKAKTRVQNQLSYKLGQALILNSKSVLGFLSLPFIILSIIISHKQEQKAYKFKV

Query: 369  NLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyikFIFKDVPR LKR
          NLALPPLETYPDYNEALKEKECFTYKLGE  I+A KNWYG GYIKF  D+  LKR
Sbjct: 519  NLALPPLETYPDYNEALKEKECFTYKLGEALIQASKNWYGGGYIKFWLIDIQNLKR
```

tr Q5W602 Putative glycosyltransferase [Campylobacter jejuni]
 Q5W602_CAMJE

Score = 219 bits (557), Expect = 2e-55

Identities = 146/357 (40%), Positives = 196/357 (54%), Gaps = 35/3

```
Query: 81  ILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYE-----VIENLKEFY
          I+  ++    + C   N  +I  N      Y   P++ + Y      + ++LK F
Sbjct: 242  IIHEDHHFGMLLCLQANKIYINLNKLY--IYRVRPNSIMNYNDNGKNINKSLKNFC

Query: 136  YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNI--KTI
          N I   K      Y      +AL +          +F+  D+I  F      N      I
Sbjct: 300  LNVIDGKKYYKILSYGINAFLALNFSN-----NFHNKDLIKLFNKAFKNECENWI

Query: 194  KDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLEN
          +  ++   S      IE  +++K+ Y+ N   L   D I          ++ INNN
Sbjct: 354  AQYPTNDLRS--LFIEIFRIMKN-YETNYENLILDFI-----AMIINNNKITIV
```


Query: 254 SINDILLTDNTPGVSFYKNQLKADNKIMLNFYINILHSDTKLIK-----FLNKEIAV
I + N + Y ++ + N I+L N +H+ +T ++ + KE +
Sbjct: 404 EIQN-----NQNTIKIYCEKINSQNNIILQQTNQIHNLNTTLENKNQLLITKENLL

Query: 309 TTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKV
+AK R+QN LSYKLGQALI+NSKSVLGFLSLPFIILSI+ISHKQEQKAYKFKV
Sbjct: 459 NYGKAKTRVQNQLSYKLGQALILNSKSVLGFLSLPFIILSIIISHKQEQKAYKFKV

Query: 369 NLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRLLK
NLALPPLETYPDYNEALKEKECFTYKLG I+A KNWYG GYIKF D+ LKR
Sbjct: 519 NLALPPLETYPDYNEALKEKECFTYKLGELIQASKNWYGGGYIKFWLIDIQNLKR

tr Q5M6Q2 Putative sugar transferase [HS23.17] [Campylobacter
Q5M6Q2_CAMJE jejuni]

Score = 214 bits (546), Expect = 3e-54
Identities = 122/188 (64%), Positives = 133/188 (69%), Gaps = 20/1

Query: 241 INNNFTLENKHNNNSI---NDILLTDNTPGVSFYKNQLKADNKIMLNFYINILHSDTK
I NN T + + N I D +LT T NQ+ N + N +L +K
Sbjct: 398 IKNNLTQDIYLNQILENKDKILTQT-----NQIYNLNTTLENKNQLLIAKQN

Query: 298 LNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISH
N +AK RIQNHLASYKLGQALIINSKSVLG+LSLPFIILSIVISH
Sbjct: 451 QNNY-----GKAKTRIQNHLASYKLGQALIINSKSVLGYLSLPFIILSIVISH

Query: 358 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIK
KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKA KNWYG GYIK
Sbjct: 502 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKASKNWYGGGYIK

Query: 418 DVPRLKRE 425
+ +LKRE
Sbjct: 562 -IKKLLKRE 568

tr Q9CLP3 Hypothetical protein PM1174 [PM1174] [Pasteurella
Q9CLP3_PASMU multocida]

Score = 213 bits (542), Expect = 9e-54
Identities = 117/248 (47%), Positives = 155/248 (62%), Gaps = 8/24

Query: 19 IIIAGNGPSLKNINYKRLPREYDVFRNCQFYFEDKYIYLGKKIKAVFFNPGVFLQY
+I+AGNG SL I+Y+ LP+ YDVFRNCQFYFE++Y+LG KIKAVFF PGVFL+QY
Sbjct: 13 VIVAGNGESLSQIDYRLLPKNYDVFRNCQFYFEERYFLGNKIKAVFFTPGVFLEQY

Query: 79 QLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNNFFPDAKLGYE-VIENLKEFYAY
L NEY + N+ S+FN P ++ + + F D GYE + L F Y
Sbjct: 73 HLKRNNEYFVDNVILSSFNHTVDL-EKSQKIQALFIDVINGYEKYLSKLTAFDVY

Query: 138 EIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYE-GDVIYPFEAMSTNIKTIFPG
E+Y N+RITSGVYMCA+AIA+GY IYL GIDFY+ + Y F+ NI + P
Sbjct: 132 ELYENQRITSGVYMCAVAIAMGYTDIYLTGIDFYQASEENYAFDNKKPNIIRLLPD

Query: 197 KP-SNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSI---NINNNFTLE
K + HSK+ D+EAL L+ Y VN Y++ S L+ HFP+ + F
Sbjct: 192 KTLFSYHSKDIDLEALSFLQQHYHVNIFYSISPMSPLSKHFPIPTVEDDCETTFVAP

Query: 253 NSINDILL 260
N INDILL
Sbjct: 251 NYINDILL 258

tr Q6EF79 Putative glycosyltransferase [Campylobacter jejuni]
Q6EF79_CAMJE

Score = 212 bits (539), Expect = 2e-53

Identities = 120/188 (63%), Positives = 133/188 (69%), Gaps = 20/1

Query: 241 INNFTLENKHNNNSI---NDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKDT
I NN T + + N I D +LT T NQ+ N + N +L +K
Sbjct: 398 IKNNLTQDIYLNQILENKDKILTQT-----NQIYNLNTTLENKNQLLIAKQN

Query: 298 LNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISH
N +AK RIQ+HLSYKLGQALIINSKSVLG+LSLPFIILSIVISH
Sbjct: 451 QNNY-----GKAKTRIQDHLSYKLGQALIINSKSVLGYLSLPFIILSIVISH

Query: 358 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIK
KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIK KNWYG GYIK
Sbjct: 502 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKASKNWWYGGGYIK

Query: 418 DVPRLKRE 425
+ +LKRE
Sbjct: 562 -IKCLKRE 568

tr Q4QNI8 CMP-Neu5Ac--lipooligosaccharide alpha 2-3 sialyltransferase
Q4QNI8_HAEI8 [lic3A]
[Haemophilus influenzae (strain 86-028NP)]

Score = 211 bits (538), Expect = 3e-53

Identities = 124/279 (44%), Positives = 161/279 (57%), Gaps = 8/27

Query: 17 QNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYYLGKKIKAVFFNPGVFLQ
+++IIAGNG SLK+I+Y LP++YDVFRCNQFYFED Y+LGKKIK VFFN V +
Sbjct: 27 KSVIIAGNGTSLKSIDYSLLPKDYDVFRCNQFYFEDHYFLGKKIKKVFFNCSVIFE

Query: 77 AKQLILKNEYEIKN---IFCSTFNLPFIESNDFLHQFYNFFPDACLGYEVIENTLKE
QLI NEY+ + I S NL H P LG+ ++ L+
Sbjct: 87 FMQLIKNNEYKYEYADIILASFLNLGDSTLKKIQH-LEKLLPQIDLGHCYLKKLRA

Query: 134 IKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFY-EGDVIYPFEAMSTNIKT
++Y+E+Y NKRITSGVYMCA+A A+GYK +YL GIDFY E Y F NI
Sbjct: 146 LQYHELYENKRITSGVYMCAVATAMGYKDLTLTGIDFYQEKGNPYAFHHQKENIIK

Query: 193 IKDFK-PSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTL
K S+ HS EYD+ AL L+ Y VNIY + +S L N+FPLS N +
Sbjct: 206 FSQNKSQSDIHSMEYDLNALYFLQKHVYGVNIYCISPESPLCNFYFPLSPLNNPIAFI

Query: 252 NNSINDILLTDN--TPGVSFYKNQLKADNKIMLNFYNIL 288
N DIL+ + Y N I F++IL
Sbjct: 266 KNYTQDILIPPKFVYKKIGIYSKPRIYQNLIFRLFWDL 304

tr Q6EF56 Putative glycosyltransferase [Campylobacter jejuni]
Q6EF56_CAMJE

Score = 207 bits (527), Expect = 5e-52

Identities = 119/188 (63%), Positives = 130/188 (68%), Gaps = 20/1

Query: 241 INNNFTLENKHNSI---NDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKDT
I NN T + + N I D +LT T NQ+ N + N +L +K
Sbjct: 398 IKNNLTQDQIYLNQILENKDKILTQT-----NQIYNLNTTLENKNQLLIAKQN

Query: 298 LNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISH
N AKARIQNHLSYKLGQALIINSKSVLG+LSLPFIILSIVISH
Sbjct: 451 QNHV-----GTAKARIQNHLSYKLGQALIINSKSVLGYLSLPFIILSIVISH

Query: 358 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEFFIKAGKNWYGEGYIK
KAYKFKV KNPNLALPPL YPDYNEALKEKECFTYKLGEFFIKA KNWYG GYIK
Sbjct: 502 KAYKFKVKNPNLALPPLVAYPDYNEALKEKECFTYKLGEFFIKASKNWWYGGGYIK

Query: 418 DVPRLKRE 425
+ +LKRE
Sbjct: 562 -IKCLKRE 568

tr Q5W603 Hypothetical protein [Campylobacter jejuni] 3
Q5W603_CAMJE a

Score = 207 bits (526), Expect = 7e-52

Identities = 121/217 (55%), Positives = 140/217 (63%), Gaps = 35/2

Query: 205 EYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLE-----NKH
+YD+E YK +IY D L N + + + N +E NK

Sbjct: 197 DYDLE-----YKESIYKNLDVQFLLNMYKEKL-FSKNKEIEKLRLSQFKKNKE

Query: 256 NDILLTDNTPGVSFYK NQLKADNKIMLN FYNILH SKDTLIKFLNKEIAVLKKQTTQ
N+I+L NQ+ N + N +L +K+ L+ F N

Sbjct: 248 NNIIILQQT-----NQIHNLTNTLENKNQLLITKENLLNFQNNY-----G

Query: 316 RIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE QKAYKFKVKKNPNLA
R+QN LSYKLGQALI+NSKSVLGFLSLPFIILSI+ISHKQE QKAYKFKVKKNPNLA

Sbjct: 291 RVQNQLSYKLGQALILNSKSVLGFLSLPFIILSIIISHKQE QKAYKFKVKKNPNLA

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYI 412
ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYG G I

Sbjct: 351 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGGGII 387

tr Q32VQ8 Hypothetical protein [Campylobacter jejuni subsp.
Q32VQ8_CAMJE jejuni]

Score = 199 bits (506), Expect = 1e-49

Identities = 144/390 (36%), Positives = 194/390 (48%), Gaps = 79/3

Query: 81 ILKNEYEIKNIFCSTFNLPFIESNDFLHQFY NFFP-DAKLG YEVIENLKEFYAYIK
I +N ++ KNI +FN +N+ + F + F + ++ +E + E +

Sbjct: 155 IYENVFKHKNI I IKSFNKDKFLNNNLIDDFLSIFKINRDSSFKTMETMNESLDIL-

Query: 140 YFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDV IYPFEAMSTNIKTI---FPG
G+ +C I D D+I + + +K + F

Sbjct: 210 -----GINICN ILYE-----DKNFSDLIIEKNLIPSFVKIMEKFFST

Query: 197 KPSNCHSKEYDIEALKLLKSIYK--VNIYALCDDSI LANHFPLSININNNFTLENK
P Y++ K +K + +N AL FP ININ + K

Sbjct: 251 LPKKTIYNNYNLFYNKEIKELENRYLNGQAL-----FP-PININ-----KYK

Query: 255 INDILLTDNTPGVSFYK-----NQLKADNKIMLN FYNILH SKDTLIKFLNK
IN+I D + F+K NQ NK N N K +++ N

Sbjct: 296 INEIKHDDFKQIILFFKEIITLILTFQNNQIQKNKEFQNIANSFPLKKQILELANL

Query: 305 LKKQTTQR-----AKARIQNHL SYKLGQALIINSKSV

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      + K+      +
Sbjct: 356 IIKKLESKKLAKSLGLKMSIINPKITFIQANS AKARIQNHL SYKLGQALI NSKS+
Query: 341 SLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLG
      +P+++ I   HK EQKAY+ K+K+NPNLALPPLETYPDYNEALKEKECFTYKLG
Sbjct: 416 RIPYVLSYIKDKHKFEQKAYEEKIKENPNLALPPLETYPDYNEALKEKECFTYKLG
Query: 401 KAGKNWYGE GYIKFIFKDVPR LKREFEKGE 430
      +A KNWYG GYIKFIFKDVPR LKREFEKGE
Sbjct: 476 QANKNWYGGGYIKFIFKDVPR LKREFEKGE 505

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tr   Q32VR3              Hypothetical protein [Campylobacter jejuni subsp.
      Q32VR3_CAMJE        jejuni]

Score = 197 bits (501), Expect = 5e-49
Identities = 116/215 (53%), Positives = 136/215 (62%), Gaps = 35/2

Query: 205 EYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLE-----NKH
      +YD+E          YK +IY   D   L N +   +   + N +E          NK
Sbjct: 197 DYDLE-----YKES IYKNLDVQFLLNMYKEKL-FSKNKEIEKLRLSQFKKNKE

Query: 256 NDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKDTLIKFLNKEIAVLKKQTTQ
      N+I+L          NQ+   N   + N   +L +K+ L+ F N
Sbjct: 248 NNIILQQT-----NQIHNLNTTLENKNQLLITKENLLNFQNNY-----G

Query: 316 RIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA
      R+QN LSYKLGQALI+NSKSVLGFLSLPFIILSI+ISHKQEQKAYKFKVKKNPNLA
Sbjct: 291 RVQNQLSYKLGQALIILNSKSVLGFLSLPFIILSIIISHKQEQKAYKFKVKKNPNLA

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE G 410
      ETYPDYNEALKEKECFTYKLGE I+A KNWYG G
Sbjct: 351 ETYPDYNEALKEKECFTYKLGEALIQASKNWYGGG 385

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tr   Q32VQ3              Hypothetical protein [Campylobacter jejuni subsp.
      Q32VQ3_CAMJE        jejuni]

Score = 197 bits (500), Expect = 7e-49
Identities = 106/156 (67%), Positives = 117/156 (74%), Gaps = 10/1

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKDTLIKFLNKEIAVLKKQTT
      I DI+ T+N   +   L+ N+ + N N +H+ +   + F N
Sbjct: 326 IADI IKTNNE-NILGLNQTL EIKNQELRNQTNQIHNLNKT LNFQNNY-----

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Query: 315 ARIQNHLASYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNL
RIQN LSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNL
Sbjct: 376 IRIQNQLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNL

Query: 375 LETYDPDYNEALKEKECFTYKLGEEFIKAGKNWYGEG 410
LETYDPDYNEALKEKECFTYKLGEEFIKA KNWYG G
Sbjct: 436 LETYDPDYNEALKEKECFTYKLGEEFIKASKNWWYGGG 471

tr Q5HT01 Capsular polysaccharide biosynthesis protein,
Q5HT01_CAMJR putative [CJE1603]
[Campylobacter jejuni (strain RM1221)]

Score = 171 bits (434), Expect = 3e-41
Identities = 87/161 (54%), Positives = 115/161 (71%), Gaps = 9/161

Query: 271 KNQLKADNKIMLNIFYNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLG
K Q K DNK + F + + + K+ ++ A R++NHL YK G
Sbjct: 493 KLGKVDNKKLNRF-----EYFFQEIMKKYKGIENNVYLSALQVRNHLCYKFG

Query: 331 INSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYDPDYNEALK
NSKS+LG++ +P+++ I HKQEQKAY+ K+K+NPALPPLETYDPDYNEALK
Sbjct: 546 ENSKSILGYIRMPYVLSHIKDKHKQEQKAYEEKIKENPNLALPPLETYDPDYNEALK

Query: 391 FTYKLGEEFIKAGKNWYGEYIKFIFKDVPRLLKRE-FEKGE 430
FTYKLG+EFIKA +NWYG GYIK +F ++ RLK+E ++KG+
Sbjct: 606 FTYKLGQEFIKASQNWYGGGYIKLLF-EIRRLKKEYYDKGK 645

tr Q5M6U5 Putative sugar transferase [HS41.06] [Campylobacter
Q5M6U5_CAMJE jejuni]

Score = 167 bits (422), Expect = 8e-40
Identities = 101/215 (46%), Positives = 126/215 (57%), Gaps = 18/2

Query: 204 KEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININ---NNFTLENKHNNSI
KEY+ L +YK I C PL I+ L+NK N +
Sbjct: 368 KEYNFNHLIPPVELYKEIIDYCTVMDPVKLAPLQKQISALTQEKQDLQNKQFQNEL

Query: 260 LTDNTPGVSFYKNQLKADNKIMLNIFYNILHSDTLIKFLNKEIAVLKKQTT----Q
+ K L+ N L SK L K L +++++ + T
Sbjct: 428 VK-----KQHLELTNLEQDLIIKKLESKK-LAKSLGLKMSIINPRITFIQAN

Query: 316 RIQNHLASYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA
RIQNHLASYKLGQALI NSKS+LG++ +P+++ I H+ EQKAY+ K+K+NPALA

Sbjct: 478 RIQNHLSYKLGQALITNSKSILGYIRMPYVLSYIKDKHQLEQKAYEEKIKENPNLA

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE 410
ETYPDYNEALKEKECFTYKLG FIKAGKNWY G

Sbjct: 538 ETYPDYNEALKEKECFTYKLGFAFIKAGKNWYRG 572

tr Q6EBB5 Tgh007 (Fragment) [Campylobacter jejuni] 1.
Q6EBB5_CAMJE a.

Score = 160 bits (404), Expect = 9e-38
Identities = 79/120 (65%), Positives = 93/120 (76%), Gaps = 1/120

Query: 308 QTTQRAKARIQNHLSYKLGQALIINSSVLFSLPFIILSIVISHKQEQKAYKFK
+T AK RIQN L Y+LGQA+IINSK+ LG++ LP+I+LSIVI +KQEQK YK K
Sbjct: 9 KTFSTAKQRIQNQLPYRLGQAMIINSKNFLGYIFLPYILLSIVILYKQEQKNYKHK

Query: 368 PNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyikfifkdvpRLK
P LPPLETYPDYNEALKEK CFTYKLG I+A K WYG GYIK FK + +LK
Sbjct: 69 PESTLPPLETYPDYNEALKEKRCFTYKLGALALIEANKKWWYGGYIKLWFK-ICKLK

tr Q4HEK5 Alpha-2,3-sialyltransferase [CC01544] [Campylobacter
Q4HEK5_CAMCO coli RM2228]

Score = 155 bits (391), Expect = 3e-36
Identities = 74/116 (63%), Positives = 91/116 (77%), Gaps = 1/116

Query: 313 AKARIQNHLSYKLGQALIINSSVLFSLPFIILSIVISHKQEQKAYKFKVKNP
AK RIQN LSYKLGQA+I NSKS+LG++ +PF++ I HKQEQK Y+ K+KK+P
Sbjct: 58 AKTRIQNQLSYKLGQAMITNSKSLGYYIRMPFVLSYIHDKHKQEQKIYQEKIKKDP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyikfifkdvpRLKREFEK
PPLE YPDY EALKEKEC TYKLGE IKA K WY GY+K F ++ +LKREF++
Sbjct: 118 PPLENYPDYKEALKEKECLTYKLGEALIKANKTWYKGGYVKMWF-EIGKLKREFKE

tr Q4HEL4 Alpha-2,3-sialyltransferase [CC01527] [Campylobacter
Q4HEL4_CAMCO coli RM2228]

Score = 153 bits (387), Expect = 9e-36
Identities = 75/146 (51%), Positives = 101/146 (68%), Gaps = 1/146

Query: 285 YNILHSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSSVLF

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      ++I      D + ++L + +A      AK RIQN LSYKLGQA+I NSKS+LG++
Sbjct: 212 FDIARPCDMISQYLLQGVAKQHVNNNGYSAKTRIQNQLSYKLGQAMITNSKSLGYI

Query: 345 IILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFI
      ++ I      HKQEQK Y+ K+KK+P+L LPPLE YPDY EALKEKEC TYKLGE I
Sbjct: 272 VLSYIKDKHKQEQKNYQEKIKKDP SLKLPLENYPDYKEALKEKECLTYKLGEALI

Query: 405 NWYGEgyikFIFKDVPR LKREFEKGE 430
      WY GY+K F ++ +L++ + + E
Sbjct: 332 TWYKGGYVKMWF-EIGKLRKRYRERE 356

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tr   Q4HEJ9      Alpha-2,3-sialyltransferase [CC01538] [Campylobacter
      Q4HEJ9_CAMCO      coli RM2228]

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Score = 145 bits (366), Expect = 2e-33
 Identities = 116/380 (30%), Positives = 178/380 (46%), Gaps = 40/3

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Query: 41  DVFRCNQFYFEDKY YLGKKIKAVFFNPGVFLQQYHTAKQLILKNEYE-IKNIFCST
      ++ N F F+ KY K + + G F + L N+++ I NI
Sbjct: 112 EILSKNHFSFQYKYLCDKNMNILVNFIFGKFEK-----LDNDFKKILNLRK

Query: 100 FIESNDFLH--QFYNFFPDALGYEVIENLKEFYAYIKYNEIYFNKRITSGVYMCA
      I + L+ +YN K+ E+ + E + Y ++ YFN I +Y+
Sbjct: 163 HINKSKHLNRYDYNS-QTYKIIREIYRDDFEIFDYDLEDKKYFN--IPQNIYLNN

Query: 158 LGYKTIYLCGIDFYEGDVIYPF-EAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALK
      + K I L + + I + + T KTI + N + + +
Sbjct: 220 ILIKNINLDSLRLKKS FQIQNLNQT IETKNKTIQENLSQINN LNQT IETKNKTIQE

Query: 217 IYKVNIYALCDD SILANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYKN
      I +N + + + N+N +NK + +N ++
Sbjct: 280 INN LNQT IETKNKTIQENLSQINN LNQT IETKNK-----TIQENLSQINN LNQ

Query: 277 DNKIMLNFYNI LHSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHL SYKLGQALIIN
      NK + N KD L+ F + AK+RIQN LSYKLGQ +I+N
Sbjct: 332 KNKTIQN-----KDDL LN F-----QAQYGTAKSRIQNQLSYKLGQTMIVN

Query: 337 LGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFT
      LG L +P I+L IVISHKQEQK YK K++K+P+L LP LE YPDY EA+K K +
Sbjct: 376 LGCLLMPVILLGIVISHKQEQKIYKQKIEKDPSLKLPSLEQYPDYREAIKLNHLS

Query: 397 EEFIKAGKNWYGEgyikFIF 416
      +E +KA K WY GY +F++
Sbjct: 436 KELVKANKIWKYKGGYFQFLY 455

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sp P24324 Hypothetical protein HI0352 (ORF1) [HI0352] 2
Y352_HAEIN [Haemophilus 2
influenzae]

Score = 129 bits (324), Expect = 2e-28

Identities = 82/186 (44%), Positives = 104/186 (55%), Gaps = 6/186

Query: 79 QLILKNEYEIKNIFCSTF-NLPFIESNDFLHQFYNFFPDACLGYEVIENLKEFYAY
QLI NEYE +I S+F NL E + +G+ + L F AY
Sbjct: 2 QLIKNEYEYADIILSSFVNLDSELKK-IKNVQKLLTQVDIGHYYLNKLPAFDAY

Query: 138 EIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFY-EGDVIYPFEAMSTNIKTIFPG
E+Y NKRITSGVYMCA+A +GYK +YL GIDFY E Y F NI + P
Sbjct: 61 ELYENKRITSGVYMCAVATVMGYKDLYLTGIDFYQEKGNPYAFHHQKENIIKLLPS

Query: 197 K-PSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLS-ININNNFTLENK
K S+ HS EYD+ AL L+ Y VNIY + +S L N+FPPLS +N F LE K
Sbjct: 121 KSQSDIHSMEYDLNALYFLQKHVGVNIYCISPESPLCNFYFPLSPLNNPITFILEEK

Query: 255 INDILL 260
DIL+
Sbjct: 181 -QDILI 185

tr Q5M6M2 Putative sugar transferase [HS19.11] [Campylobacter
Q5M6M2_CAMJE jejuni]

Score = 124 bits (310), Expect = 7e-27

Identities = 68/151 (45%), Positives = 93/151 (61%), Gaps = 4/151

Query: 270 YKNQLKADNKIMLNIFYNILHSKDTLIKFLNKEIAVLKKQTTQR----AKARIQNHL
YK+ L + K+ + + I D + F+N + K Q AK RIQN L
Sbjct: 346 YKDILFENIKLNQDPWAIKDKIDIINFFVNNKFKDNKYQFNTNLYGTAKQRIQNQL

Query: 326 GQALIINSKSVLGFSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY
GQ +IINSKS++G L +P +LS +++KQ+QK Y K+KK+P L LPPL E YPDY
Sbjct: 406 GQTMIIINSKSIIGILFMPYIYLLSTFLNYKQDQKIYHQKIKKDPTLKLPLENYPDY

Query: 386 KEKECFYTKLGEEFIKAGKNWYGEYIKFIF 416
K KE +YKLG+ +++ K W+ G KF F
Sbjct: 466 KYKEHLSYKLGKILLESFKTWHKGGFLFKFPF 496

tr Q5M6M5 Putative sugar transferase [HS19.08] [Campylobacter
Q5M6M5_CAMJE jejuni]

Score = 122 bits (306), Expect = 2e-26
Identities = 58/104 (55%), Positives = 75/104 (71%)

Query: 313 AKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP
AK RIQN L YKLGQ +IINSKS++G L +P +LS +++KQ+QK Y K+KK+P
Sbjct: 390 AKQRIQNQLCYKLGQTMIIINSKSIIGILFMPPIYLLSTFLNYKQDQKIYHQIKKDP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIF 416
PPLE YPDY EALK KE +YKLG+ +++ K W+ G KF F
Sbjct: 450 PPLENYPDYQEALKYKEHLSYKLGKILLESFKTWHKGGFLFKFPF 493

tr Q5HT02 Capsular polysaccharide biosynthesis protein,
Q5HT02_CAMJR putative [CJE1602]
[Campylobacter jejuni (strain RM1221)]

Score = 120 bits (301), Expect = 8e-26
Identities = 66/197 (33%), Positives = 111/197 (55%), Gaps = 24/19

Query: 240 NINNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKDT--
+I NF +E+++ + N ++ D ++ L+ N+ DT
Sbjct: 450 SIKPNFKIEHRYTKAQNQGYIMPD-----ISKELYLDLLNLRDKFDTKK

Query: 298 LNKEIAVLKKQTTQR-----AKARIQNHLASYKLGQALIINSKSVLGFLSLPFI
+ V KK ++ AK+RI+NHL+Y+ G +I S+++LG++ +PFI
Sbjct: 497 IYFFQKVTKKYCKEKLTDVYFSAKSRIKNHLAYQFGLTMIQYSRNILGYVKMPFI

Query: 350 VISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKN
++ ++K Y ++ +NP LP ++ Y DY EA+K KE TY+LG+ I+A KN
Sbjct: 557 FRQYQNKKKEYYERISENPKFILPKIKEYADYQEAIKLKESITYRLGQALIQANKN

Query: 410 GYIKFIFKDVPRCLKREF 426
GYIK +F ++ RLK+E+
Sbjct: 617 GYIKLLF-EIRRLKKEY 632

tr Q4HR89 Hypothetical protein [CUP1274] [Campylobacter
Q4HR89_CAMUP upsaliensis RM3195]

Score = 115 bits (287), Expect = 3e-24
Identities = 72/196 (36%), Positives = 109/196 (54%), Gaps = 22/19

Query: 241 INNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSKDTLIK
IN + LE K ++L +N + ++KA K+ L +++ L+K
Sbjct: 190 INKAYELEQK-----TGVVLKNNKEEKKILQ-KIKAQEKL-----LRTQNLLLK

Query: 301 EI-----AVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILS
+ A + Q + A R+ HL+YKLG A+I+ SKS+LG+ +PF++
Sbjct: 237 QAKPNNPSPQAQIPLQKPKGAVERVHRHLAYKLGIAIIVCSKSLGAYRMPFVLYH

Query: 353 HKQEQQAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYG
HK EQ+ ++ + KNP L L PLE+Y DY ALKE+ C+TYKLG ++A +N +
Sbjct: 297 HKFEQEKFKALLKNPTLKLPLESYADYENALKEQRCYTYKLGGLAMMEAHRNLFK

Query: 413 KFIFKDVPRLLKREFEK 428
F F+ RLKREFEK
Sbjct: 357 WIFYFES-KRLKREFEK 371

tr Q4HEL1 DcbE, putative [CC01537] [Campylobacter coli
Q4HEL1_CAMCO RM2228]

Score = 107 bits (266), Expect = 9e-22
Identities = 65/143 (45%), Positives = 88/143 (61%), Gaps = 14/143

Query: 274 LKADNKIMLNF-YNILHSDKDTL-----IKFLNKEIAVLKKQTTQRAKARIQ
LK+ NK +L+F ++I + L IK N ++ K T AK RIQ
Sbjct: 247 LKSKNKSLLDFFIDIQEDLEKLHQENCRLEAHIKNQNSLLSFCMKYGT--AKQRIQ

Query: 323 YKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQQAYKFKVKKNPNLALPPLETY
Y+LGQ IINSK++ L +P +LS +IS KQE++ Y K+KK+P+L LPPLE Y
Sbjct: 305 YRLGQT-IINSKNIFKILFMPIFLLSNIISFKQERQVYNKKIKKDPSSLILPPLEKY

Query: 383 EALKEKECFTYKLGEEFIKAGKN 405
EA+K K +Y+LG+ IK KN
Sbjct: 364 EAIKFKNYLSYRLGQVVIKGFKN 386

Score = 34.7 bits (78), Expect = 5.8
Identities = 15/51 (29%), Positives = 30/51 (58%)

Query: 305 LKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQ 355
L+K + + +N+LSY+LGQ +I K+ L + LP+ I+ ++ ++
Sbjct: 356 LEKYPDYQEAIKFKNYLSYRLGQVVIKGFKNPLSIILLPYEIVKLIYKFRK 406

tr Q9PMM6 Hypothetical protein Cj1431c [Cj1431c]
Q9PMM6_CAMJE [Campylobacter jejuni]

Score = 99.4 bits (246), Expect = 2e-19

Identities = 63/148 (42%), Positives = 88/148 (58%), Gaps = 13/148

Query: 283 NFYNILHSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLGGQALIINSKSVLG
 NF+ I+ D F+ K++ K A +I+NHL+YKLG A I NSKS+ G
 Sbjct: 448 NFHPIIF--DQFKMFIFKDLP--KSDQEIGAVKKIRNHLAYKLGVAAIKNSKSLWG

Query: 343 PFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEE
 P+++ I HK+ Q KK+ +L E Y DY ALKEKE F YKLG+
 Sbjct: 504 PYVLSYIRDMHKESQNKMD---KKSISL-----EYYS DYESALKEKEGFVYKLGQI

Query: 403 GKNWYGEgyIKFIFKDVPRLKREFEKGE 430
 KNW+ GYI F +V +LK+EF+KG+
 Sbjct: 556 HKNWHKGGYIMLWF-EVKKLKKEFKKGK 582

tr Q50FV9 Cj81-063 (Fragment) [Campylobacter jejuni] 56 A
 Q50FV9_CAMJE align

Score = 99.0 bits (245), Expect = 3e-19

Identities = 47/56 (83%), Positives = 49/56 (86%), Gaps = 1/56 (1%)

Query: 370 LALPPLETYPDYNEALKEKECFTYKLGEFEIKAGKNWYGEgyIKFIFKDVPRLKRE
 LALPPLETYPDYNEALKEKECFTYKLGEFEIKA KNWYG GYIK K + +LKRE
 Sbjct: 1 LALPPLETYPDYNEALKEKECFTYKLGEFEIKASKNWYGGGYIKLRLK-IKKLKRE

tr Q4HR98 Hypothetical protein [CUP1265] [Campylobacter
 Q4HR98_CAMUP upsaliensis RM3195]

Score = 97.1 bits (240), Expect = 1e-18

Identities = 49/116 (42%), Positives = 76/116 (65%), Gaps = 9/116

Query: 311 QRAKARIQNHLASYKLGGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKK
 Q A +++HL+YKLG +I NSKS+LG + +P+++++I +H +E+K +
 Sbjct: 447 QGAIKLVKSHLAYKLGACMIRNSKSLGCIKMPYLLVAIKWAHAERKNF-----

Query: 371 ALPPLETYPDYNEALKEKECFTYKLGEFEIKAGKNWYGEgyIKFIFKDVPRLKREF
 + PL+ Y DY EALK KE +YKLGE IKA KN + G IKF+FK+ ++R+F
 Sbjct: 498 NITPLQDYIDYEEALKVKEFLSYKLGEALIKAYKNMWKGGLIKFVFKEAWEIRRDF

tr Q4HKU2 Glycosyl transferase family 8 family [CLA1010] [Campylobacter
 Q4HKU2_CAMLA lari
 RM2100]

Score = 90.9 bits (224), Expect = 7e-17

Identities = 50/122 (40%), Positives = 73/122 (58%), Gaps = 6/122

Query: 307 KQTTQRAKARIQNHLASYKLGQALIINSSVLSGLSLPFIILSIVISHKQEQKAYKF
KQ+ QR K HLSYKLG A I +K+ LPF +L I H + K Y+

Sbjct: 281 KQSIQRTKY----HLSYKLGAFIECTKNKKKIPFLPFTLLKIYYKHTKLAKQYQK

Query: 367 NPNLALPPLETYPDY-NEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPR
P L LPPL +Y DY +E +K + ++YK+G+ IKA +NW+ GY+KFI K++

Sbjct: 337 KPYLKLPLSSYDDYKSEGIKNQNTYSYKIGQALIKAQRNWHKGGYVKFI-KELKH

Query: 426 FE 427

++

Sbjct: 396 YK 397

tr Q5M6U6 Putative sugar transferase [HS41.05] [Campylobacter
Q5M6U6_CAMJE jejuni]

Score = 89.7 bits (221), Expect = 2e-16

Identities = 46/112 (41%), Positives = 73/112 (65%), Gaps = 1/112

Query: 316 RIQNHLASYKLGQALIINSSVLSGLSLPFIILSIVISHKQEQKAYKFKVKKNPNL
R++NHL+YKLGQ +I + + G+++L + I HK+EQK YK ++ P L

Sbjct: 10 RVKNHLAYKLGQVMIDFANNGGGYIALFKKLYKIKKQHKKEQKIYKQTIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPRLKREFE 427
ET PDY+E+L+ K +Y LGE IKA N + +GY F+FK++ + K++++

Sbjct: 70 ETCPDYSESLRYKFHLSYMLGEVLIKADMNKFKDGYF-FLFKNIEQTKKDYK 120

tr Q5M6S8 Putative sugar transferase [HS41.23] [Campylobacter
Q5M6S8_CAMJE jejuni]

Score = 89.4 bits (220), Expect = 2e-16

Identities = 64/214 (29%), Positives = 107/214 (49%), Gaps = 31/21

Query: 201 CHSKEYDIEALKLLKSIYKV-----NIYALCDDSI LANHFPLSININNNFTL
C+SKE +A K +K ++ N+Y+ DD ++

Sbjct: 247 CYSKEEFKAFKKIKILHYTYLYMPKPWENVYSFIDDDYNLVYY-----

Query: 252 NNSINDILLTDNTPGVSFYKNQLKADNKIMLNfYNILHskDTLIKFLNKEI----A
++ D+ L G F K + + + K +L + + K IK L K+

Sbjct: 293 YDAWWDMAKTPIIYGEHFAKKKREYEKSLTYAQAMSK---IKALEKKTENN

Query: 308 QTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFK
 T A R++NHL+YK+G+ LI N +VL L +PF ++ +++ HK YK
 Sbjct: 350 CLTNGACDRVKNHNLNYKIGRVLIDNF-TVLKILLIPFKLIYVIMIHKISSFIYKIL

Query: 368 PNLALPPLETYPDYNEALKEKECFTYKLGEEFIK 401
 P+L L PLE Y DY EA++ K F+Y+LG+ F+K
 Sbjct: 409 PSLKLLPLEKYADYEEAMRIKSFFSYRLGKLFLK 442

tr Q6EF57 Putative glycosyltransferase (Putative sugar transferase)
 Q6EF57_CAMJE [HS23.16]
 [Campylobacter jejuni]

Score = 85.1 bits (209), Expect = 4e-15
 Identities = 74/222 (33%), Positives = 105/222 (46%), Gaps = 27/22

Query: 214 LKSIYKVNIYALCDDASILANHFPLSININNNFTLENKHNNNSI----NDILLT---D
 +K + K IY L +D H + NN F + ++ + I DI L+
 Sbjct: 359 IKYLKKALIYDLNDNDKYRI-HIIYMLLCNNKFKILERYLSIIMSyrKDIFLSTLFS

Query: 267 VSFYKNQLKADNKIMLNFYNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNHL
 Y N L YNI + + + I + A ++ HLS
 Sbjct: 418 GYVYLNILSDFLNYSQRIYNIKYLYPNIFYIITEIIKL-----NLFAVFLVKQHLS

Query: 327 QALIINSKSVLGFLSLPFIILSIVISHKQEQKA-YKFKVKKNPNLALPPLETYPDY
 + I+ +KS+L + LP + +IV SHK+ Q Y K+ E DY
 Sbjct: 473 KR-IVQTKSILDIIELPLDLKNIVDSHKRNQLIPYNIKI-----ENCLDY

Query: 386 KEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVRLKREFE 427
 K K F+YKLG IKA KNWY GYIKF F D+ +LK+E++
 Sbjct: 521 KIKNYFSYKLGLILIKAHKNWYKGGYIKFWF-DLYKLKKEYK 561

tr Q4HR96 Glycosyl transferase, group 2 family protein
 Q4HR96_CAMUP [CUP1267]
 [Campylobacter upsaliensis RM3195]

Score = 85.1 bits (209), Expect = 4e-15
 Identities = 52/143 (36%), Positives = 81/143 (56%), Gaps = 10/143

Query: 287 ILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSL
 IL+SK + + + + K A RI+N LSYKLG+A I+ + S L FL L
 Sbjct: 336 ILNSKDPNLNLRVRECVKIQKYIKENGaidRIKNQLSYKLGEA-ILKANSPLKFLKL

Query: 347 LSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKA

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      +S+  +H+  EQK  +F  ++  P      LE Y DY EAL+ K+  +Y+LG+  +K
Sbjct: 395 ISLAKTHQFEQKVLQFLIRLEPKFKPLDLEKYADYEEALRIKKHLSYRLGQALLK-
Query: 407 YGEGYIKFIFKDVPRLLKREFEKG 429
      + FIFK +P + + F+KG
Sbjct: 450 ---NPLTFIFK-IPSIYQNFKKG 468

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tr    Q4HLH9          Hypothetical protein [CLA0678] [Campylobacter lari
      Q4HLH9_CAMLA    RM2100]

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Score = 84.0 bits (206), Expect = 8e-15

Identities = 120/485 (24%), Positives = 198/485 (40%), Gaps = 81/4

```

Query: 4   TRMENELIVSKNMQNI IIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKY YLGKK
          T ++N   + ++ + II +   S  NIN   P   +   N  YF ++ Y   K
Sbjct: 37  TSLQONLYELMRHEKTI IKSDFI ISES NINDYLS PMSLSIILRNIDYFY EELYKANK

Query: 64  FFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFI E---SND FLHQF---YNF
          P   +   +   + I  NE  KN   FNL  ++   + L+ F   Y  F
Sbjct: 97  LILP---IPACNDKSKAI--NEAHRKNCAYYG FNLI DV DLYYQKNNLYDFDQNYKF

Query: 118  ----KLG YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCG--
          +LG  +I+NL  F   K  E   +   ++  + +  + +K  + C
Sbjct: 152  LAMQELGKNIIKNLHNFK---KSKENI ICSKRKYHIFT PSNSTKIEHKNSFFCEKI

Query: 170  FYEGDVIYPFEAMSTNIKTIFPGIKDFKPSNCH---SKEYDIEALKLLKSIYKVNI
          E  +I+P E   I  I   +   S+ H   S   + KL+K+   +N
Sbjct: 209  ASE-KIIFPKELKGHQILGIHTW--NHASSSTHAISSISIKNSSFKLVKNFGLINT

Query: 224  ----ALCDDS-----ILANHFP L SININNNFT-----LENKHNN
          A+CD+   I   +   ++I N  T   LEN ++
Sbjct: 266  QNEKAICDEQTFLYINTQIIKQSEESSGLSIANEKTPRLDYVDLIGILLLENDNDK

Query: 258  ILLTDNT-----PGVSFYKNQLKADNKIM-LNFYNILHSDK-TLIKFLNK-----
          NT   P ++FYK  +   +++  L+   L S++  L++FLN
Sbjct: 326  KNYLTNTHELLIPPIAFYKELVLEYHELKKLDMQTFLQSQNHNLRLFLNHKGLKNE

Query: 304  VLKKQTTQRAKARIQNHL SYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE QKA
          + +   A  RI+  LSYKLG+A++ NSKS LG+  +PF +  +   H + QK
Sbjct: 386  IHQNNKLYGASLRIKERLSYKLG EAIMKNSKSYLGYFKIPFELRKVKKEHFKNQKD

Query: 364  VKKNPNLALPPLETYPDYNEALKEKECF TYKLGE EFIKAGKNWYGE GYIKFIFKDV
          LPPL+ Y DY  A   K   Y LG  ++A +  +  GY+  FK  +
Sbjct: 444  -----NL PPLKAYADYKHAQIAKTHLPYLLGNALLQASRTPFKIGYLTLPFK-L

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Query: 424 REFEEK 428
+ ++K
Sbjct: 496 KNYKK 500

tr Q9PMN6 Possible sugar transferase [Cj1421c] [Campylobacter
Q9PMN6_CAMJE jejuni]

Score = 82.8 bits (203), Expect = 2e-14
Identities = 45/112 (40%), Positives = 69/112 (61%), Gaps = 1/112

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA
R++NHL+YKLGQ +I + + G+++L + I HK+EQK Y+ ++ P L
Sbjct: 10 RVKNHLAYKLGQTVIEHRHNGGGYIALFKKLYKIKKQHKKEQKIYQQIIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRLKREFE 427
ET DYNEAL+ K +Y +GE IKA +NWY G K + ++ + +EF+
Sbjct: 70 ETCSDYNEALRCKFHLSYMIGEVLIKAYQNWYKGGGFK-LKNNIKKANKEFQ 120

tr Q9PMN5 Possible sugar transferase [Cj1422c] [Campylobacter
Q9PMN5_CAMJE jejuni]

Score = 82.8 bits (203), Expect = 2e-14
Identities = 45/112 (40%), Positives = 69/112 (61%), Gaps = 1/112

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA
R++NHL+YKLGQ +I + + G+++L + I HK+EQK Y+ ++ P L
Sbjct: 10 RVKNHLAYKLGQTVIEHRHNGGGYIALFKKLYKIKKQHKKEQKIYQQIIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRLKREFE 427
ET DYNEAL+ K +Y +GE IKA +NWY G K + ++ + +EF+
Sbjct: 70 ETCSDYNEALRCKFHLSYMIGEVLIKAYQNWYKGGGFK-LKNNIKKANKEFQ 120

tr Q6EF89 Putative glycosyltransferase [Campylobacter jejuni]
Q6EF89_CAMJE

Score = 81.6 bits (200), Expect = 4e-14
Identities = 46/113 (40%), Positives = 69/113 (60%), Gaps = 3/113

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA
R++NHL+YKLGQA+I + + G+++L + I HK+EQK Y+ ++ P L
Sbjct: 10 RVKNHLAYKLGQAMIEFTNNGGGYIALFKKLYKIKKQHKKEQKIYQQTIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEGYIKFIFKDVPRCLKREFE 42
ET DY +ALK K +Y LGE IKA K W+ G G+ + D+ + +EF+
Sbjct: 70 ETCSDYEQALKYKFHLSYMLGEVLIKADKTWHKGS GF--KLKNDIKKANKEFK 12

tr Q6EF76 Putative glycosyltransferase [Campylobacter jejuni]
Q6EF76_CAMJE

Score = 81.6 bits (200), Expect = 4e-14
Identities = 46/113 (40%), Positives = 69/113 (60%), Gaps = 3/113

Query: 316 RIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA
R++NHL+YKLGQA+I + + G+++L + I HK+EQK Y+ ++ P L
Sbjct: 10 RVKNH LAYKLGQAMIEFTNNGGGYIALFKKLYKIKKQHKKEQKIYQQTIQVFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEGYIKFIFKDVPRCLKREFE 42
ET DY +ALK K +Y LGE IKA K W+ G G+ + D+ + +EF+
Sbjct: 70 ETCSDYEQALKYKFHLSYMLGEVLIKADKTWHKGS GF--KLKNDIKKANKEFK 12

tr Q5M6M6 Putative sugar transferase [HS19.07] [Campylobacter
Q5M6M6_CAMJE jejuni]

Score = 81.6 bits (200), Expect = 4e-14
Identities = 48/115 (41%), Positives = 70/115 (60%), Gaps = 5/115

Query: 316 RIQNHL SYKLGQALI--INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPN
R++NHL+YKLGQA+I NS S G+++L + I HK+EQK Y+ ++ P
Sbjct: 10 RVKNH LAYKLGQAMIDFANSSSGGGYIALFKKLYKIKKQHKKEQKIYQQTIQVFPQ

Query: 374 PLETPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEGYIKFIFKDVPRCLKREFE
LE DY +ALK K +Y LGE IKA +NWY G G+ + ++ + +EF+
Sbjct: 70 SLEACSDYEQALKYKFHLSYMLGEVLIKAYQNWYKGAGF--KLKNNIKKANKEFQ

tr Q9PMM3 Putative sugar transferase [Cj1434c] [Campylobacter
Q9PMM3_CAMJE jejuni]

Score = 81.3 bits (199), Expect = 5e-14
Identities = 41/95 (43%), Positives = 61/95 (64%), Gaps = 1/95 (1%)

Query: 313 AKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP
A+AR+QN L Y+LG+ +++ +KS + LPF++L I + H E K Y+ V+ P

Sbjct: 329 ARARLQNQLVYRLGK-VVVEAKSFNKIIKLPFLMLKICLEHNFEHKVYRSIVQFRP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEFEIKAGKNWY 407

PLE Y DY+EAL KE +YK G+ + + K WY

Sbjct: 388 LPLECYLDYHEALVIKEHLSYKFGKLILLSFKGWY 422

tr Q4HR95 Glycosyl transferase, group 2 family protein,
Q4HR95_CAMUP putative [CUP1268]
[Campylobacter upsaliensis RM3195]

Score = 80.9 bits (198), Expect = 7e-14

Identities = 46/114 (40%), Positives = 69/114 (60%), Gaps = 10/114

Query: 316 RIQNHLASYKLGQALIINSSVGLFSLPFIILSIVISHKQEQKAYKFKVKKNPNLA

RI+N LSYKLG+A I+ + S L FL LPF ++S+ +H+ EQK +F ++ P

Sbjct: 343 RIKNQLSYKLGEA-ILKANSPKFLKLPFTLISLAKTHQFEQKVLQFLIRLEPKFK

Query: 376 ETYPDYNEALKEKECFTYKLGEFEIKAGKNWYGEGYIKFIFKDVPRKREFEKG 4

E Y DY EAL+ K+ +Y+LG+ +K + FIEK +P + + F+KG

Sbjct: 402 EKYADYEEALRIKKHLSYRLGQALLK-----NPLTFIFK-IPSIYQNFKKG 4

tr Q5M6R2 Putative sugar transferase [HS23.07] [Campylobacter
Q5M6R2_CAMJE jejuni]

Score = 80.1 bits (196), Expect = 1e-13

Identities = 45/113 (39%), Positives = 69/113 (60%), Gaps = 3/113

Query: 316 RIQNHLASYKLGQALIINSSVGLFSLPFIILSIVISHKQEQKAYKFKVKKNPNLA

R++NHL+YKLGQA+I + + G+++L + I HK+EQK Y+ ++ P L

Sbjct: 10 RVKNHLAYKLGQAMIEFTNNGGGYIALFKKLYKIKKQHKKEQKIYQQTIIQIFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEFEIKAGKNWY-GEGYIKFIFKDVPRKREFE 42

ET DY +AL+ K +Y LGE IKA K W+ G G+ + D+ + +EF+

Sbjct: 70 ETCGDYEQALRYKFHLSYMLGEVLIKADKTWHKGSFG--KLKNDIKKANKEFK 12

tr Q5M6P9 Putative sugar transferase (Cj81-080) [HS23.20]
Q5M6P9_CAMJE [Campylobacter
jejuni]

Score = 80.1 bits (196), Expect = 1e-13

Identities = 45/113 (39%), Positives = 69/113 (60%), Gaps = 3/113

Query: 316 RIQNHLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLA
R++NHL+YKLGQA+I + + G+++L + I HK+EQK Y+ ++ P L
Sbjct: 10 RVKNHLAYKLGQAMIEFTNNGGGYIALFKKLYKIKKQHKKEQKIYQQTIQIFPQLK

Query: 376 ETYPDYNEALKEKECFTYKLGEEFIKAGKNWY-GEGYIKFIFKDVPRCLKREFE 42
ET DY +AL+ K +Y LGE IKA K W+ G G+ + D+ + +EF+
Sbjct: 70 ETCGDYEQALRYKFHLSYMLGEVLIKADKTWHKGS GF--KLKNDIKKANKEFK 12

tr Q4HRA0 Glycosyl transferase family 8 family [CUP1263]
Q4HRA0_CAMUP [Campylobacter
upsaliensis RM3195]

Score = 77.8 bits (190), Expect = 6e-13

Identities = 49/117 (41%), Positives = 67/117 (56%), Gaps = 1/117

Query: 309 TTQRAKARIQNHLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKV
T A R++NHL+YKLG+ LI NS + L F + + + +K E K K
Sbjct: 396 THNDALRRVKNHLAYKLGE-LIQNSNFSILSLKFLFKAVKLYLQNKTEIKIAKNCS

Query: 369 NLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRCLKR
L PLE +Y EALK K+ TY+LGE FIK+ + G G IKF FK++P+ +
Sbjct: 455 FLKFLPLEHCFNYEEALKMKQNLTYRLGEAFIKSLTHTGGGGVIKFYFKELPKFHK

tr Q4HSD1 Probable sugar transferase Cj1422c [CUP0322]
Q4HSD1_CAMUP [Campylobacter
upsaliensis RM3195]

Score = 77.0 bits (188), Expect = 1e-12

Identities = 45/112 (40%), Positives = 65/112 (57%), Gaps = 1/112

Query: 313 AKARIQNHLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP
A RI+NHLSYKLGQ LI + G +SL F + I +H + K Y+ ++ P
Sbjct: 8 ATQRIKNHLSYKLGQELIKYNTGGGGVISLLFKLYHIKKTTHHKYKLIYQQIIEVFP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEYIKFIFKDVPRCLKR 424
PPL+ DY + L+ + +Y LG+ IKA K WY GY+K + K++ KR
Sbjct: 68 PPLKQCEDYQQGLQCQFHL SYLLGKALIKADKAWYKGGYK-LSKEIKEAKR 118

tr Q4HQ44 Probable sugar transferase Cj1422c [CUP1233]
Q4HQ44_CAMUP [Campylobacter
upsaliensis RM3195]

Score = 77.0 bits (188), Expect = 1e-12

Identities = 45/112 (40%), Positives = 65/112 (57%), Gaps = 1/112

Query: 313 AKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP
A RI+NHLSYKLGQ LI + G +SL F + I +H + K Y+ ++ P
Sbjct: 8 ATQRIKNHLASYKLGQELIKYNTGGGGVISLLFKLYHIKKTTHHKYLKIYQQIIEVFP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIFKDVPRLLKR 424
PPL+ DY + L+ + +Y LG+ IKA K WY GY+K + K++ KR
Sbjct: 68 PPLKQCEDYQQGLQCQFHLASYLLGKALIKADKAWYKGGYK-LSKEIKEAKR 118

tr Q4HLH0 Probable sugar transferase Cj1422c [CLA0667]
Q4HLH0_CAMLA [Campylobacter lari
RM2100]

Score = 76.3 bits (186), Expect = 2e-12

Identities = 45/99 (45%), Positives = 59/99 (59%), Gaps = 4/99 (4%)

Query: 316 RIQNHLASYKLGQALIINSKSVLG---FLSLPFIILSIVISHKQEQKAYKFKVKKNP
RI+N LSYKLG A II K G +++LP+ + I H +EQK YK +K P
Sbjct: 10 RIKNSLSYKLGLA-IIECKKQHGRGRYITLPYKLYKIKQQHFKEQKLYKQTIKIFP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGY 411
P +E+ DYNE+++ K +Y LGE I A K WY GY
Sbjct: 69 PKVESCKDYNESIRYKYHLSYMLGEALICAHKAWYKGGY 107

tr Q4HLF9 Probable sugar transferase Cj1421c [CLA0655]
Q4HLF9_CAMLA [Campylobacter lari
RM2100]

Score = 76.3 bits (186), Expect = 2e-12

Identities = 45/99 (45%), Positives = 59/99 (59%), Gaps = 4/99 (4%)

Query: 316 RIQNHLASYKLGQALIINSKSVLG---FLSLPFIILSIVISHKQEQKAYKFKVKKNP
RI+N LSYKLG A II K G +++LP+ + I H +EQK YK +K P
Sbjct: 10 RIKNSLSYKLGLA-IIECKKQHGRGRYITLPYKLYKIKQQHFKEQKLYKQTIKIFP

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGY 411
P +E+ DYNE+++ K +Y LGE I A K WY GY
Sbjct: 69 PKVESCKDYNESIRYKYHLSYMLGEALICAHKAWYKGGY 107

tr Q4HNW9 Capsular polysaccharide biosynthesis protein,
Q4HNW9_CAMUP putative [CUP0185]
[Campylobacter upsaliensis RM3195]

Score = 75.9 bits (185), Expect = 2e-12

Identities = 46/113 (40%), Positives = 66/113 (57%), Gaps = 2/113

Query: 313 AKARIQNHLASYKLGQALI-INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKN
A RI+NHLSYKLGQ LI N+ G +SL F + I +H + K Y+ ++

Sbjct: 8 ATQRIKNHLASYKLGQELIKYNTGGGGVISLLFKLYHIKKTTHKYLKIYQQIIEVF

Query: 372 LPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPR LKR 42
PPL+ DY + L+ + +Y LG+ IKA K WY GY+K + K++ KR

Sbjct: 68 YPPLKQCEDYQQGLQCQFHL SYLLGKALIKADKAWYKGGYLK-LSKEIKEAKR 11

tr Q9PML9 Putative sugar transferase [Cj1438c] [Campylobacter
Q9PML9_CAMJE jejuni]

Score = 75.1 bits (183), Expect = 4e-12

Identities = 46/116 (39%), Positives = 68/116 (57%), Gaps = 10/116

Query: 313 AKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP
A RI+ LSY++G+ L+I+ K+ + L PF + + K EQK YK +K P

Sbjct: 338 ASERIKWQLSYRIGK-LLIDLKNPVQILKFPFKLFLEIKQFKFEQKIYKTTIKFYF

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPR LKREFEK
PPLE Y DY +ALK K+ +Y LG+ FI I FIFK + ++ ++++K

Sbjct: 397 PPLEEYSDYEQALKTKKHL SYILGKSFI-----NNPILFIFK-IKKIYKQYKK

tr Q4HQ73 Capsular polysaccharide biosynthesis protein,
Q4HQ73_CAMUP putative [CUP1137]
[Campylobacter upsaliensis RM3195]

Score = 74.7 bits (182), Expect = 5e-12

Identities = 47/140 (33%), Positives = 74/140 (52%), Gaps = 2/140

Query: 271 KNQLKADNKIMLNFYNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLG
+N K K +F+ L+S +K K K +R KA + L ++L

Sbjct: 300 QNYPKEKLKEFESFFEELNSHLKSLKIHRKYFYYNKTLADERIKATLT YRLGFELV

Query: 331 INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALK
+++++ F++LP+ +L I HK E++ Y+ +K NP L+LPPLE DY +AL

Sbjct: 359 -KNRNLVDFIALPYRL LKIKLHKIEKENYQKA IKINPKLSLPPLEHCADYEKALY

Query: 391 FTYKLGEEFIKAGKNWYGEG 410
+YK+GE F+KA G G
Sbjct: 418 LSYKVGESFLKACNTGGGGG 437

tr Q9PMM5 Putative sugar transferase [Cj1432c] [Campylobacter
Q9PMM5_CAMJE jejuni]

Score = 73.6 bits (179), Expect = 1e-11
Identities = 37/113 (32%), Positives = 67/113 (58%), Gaps = 5/113

Query: 317 IQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPDLA
I++HLSYKLG+ +++N K+ L ++ L +I ++ SH +++K Y + K N +L+
Sbjct: 924 IKSHLSYKLGKVILLNIKNPLKWIKLIVLIPILIFSHHEQKKIYLTEKKINIDLS

Query: 377 TYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIFKDVPRLLKREFEKG 4
Y DYNEA+ + F+Y+LGE +K + W + +K +++F+KG
Sbjct: 980 -YKDYNEAIMVRNFFSYQLGELILKTSRKWNVLAIVILPYKIAQLYRKKFKKG 1

tr Q4HTL3 Hypothetical protein [CUP0667] [Campylobacter
Q4HTL3_CAMUP upsaliensis RM3195]

Score = 71.6 bits (174), Expect = 4e-11
Identities = 50/130 (38%), Positives = 69/130 (52%), Gaps = 22/130

Query: 298 LNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISH
L EI LK + Q IQ HL++KLG+A+I N S GFL LPF++ I +
Sbjct: 407 LQAEIENLKCELNQFKVNPIQTHLAHKLGRAIIENYGSFWGFLGLPFVLNYIAKKY

Query: 358 KAYKFKVKKNPDLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIK
LP E+ EK+ F+Y+LG IKA K WY GY+
Sbjct: 467 N-----ILPCDES-----EKQIFSYQLGLALIKAHKAWYKGGYVW

Query: 418 DVPRLKREFE 427
++ RLK++F+
Sbjct: 505 EIFRLKKKFK 514

tr Q5M6N9 Putative sugar transferase [HS1.07] [Campylobacter
Q5M6N9_CAMJE jejuni]

Score = 68.2 bits (165), Expect = 5e-10
Identities = 43/118 (36%), Positives = 68/118 (57%), Gaps = 7/118

Query: 316 RIQNHLASYKLGQALII-----NSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVK
RI+NHL+YKLG+ +I N K G+++L + I HK+EQK Y+ ++
Sbjct: 10 RIKNHLAYKLGKVMIDFSHQNNYKYGGGYIALFKKLYKIKKQHKKEQKIYQQTIQ

Query: 370 LALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIFKDVPRKRE
L P LET DY +ALK K +Y LGE I+ +N + +G + + K++ + +E
Sbjct: 70 LKYPNLETCSDYEQALKYKFHLSYMLGEVLIQTFQNLH-KGSMFKLAKNIKKANKE

tr Q50FW8 Cj81-047 (Fragment) [Campylobacter jejuni] 1
Q50FW8_CAMJE a

Score = 66.2 bits (160), Expect = 2e-09
Identities = 42/97 (43%), Positives = 53/97 (54%), Gaps = 13/97 (1

Query: 332 NSKSVLGFLSLPFIILSIVISHKQEQKA-YKFKVKKNPNLALPPLETYPDYNEALK
N L + LP + +IV SHK+ Q Y K+ E DY EALK
Sbjct: 95 NQNQFLDIIEPLDLKNIVDSHKRNQLIPYNIKI-----ENCLDYGEALK

Query: 391 FTYKLGEEFIKAGKNWYGEGYIKFIFKDVPRKREFE 427
F+YKLG IKA KNWY GYIKF F D+ +LK+E++
Sbjct: 144 FSYKLGLILIKAHKNWYKGGYIKFWF-DLYKCLKKEYK 179

tr Q5M6S9 Putative sugar transferase [HS41.22] [Campylobacter
Q5M6S9_CAMJE jejuni]

Score = 63.2 bits (152), Expect = 2e-08
Identities = 33/89 (37%), Positives = 52/89 (58%), Gaps = 1/89 (1%

Query: 313 AKARIQNHLASYKLGQALIINNSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNP
A RI+ +LSYK+G I+ +K++L F +LP+ +L ++ H+ YK K+K N
Sbjct: 605 AALRIKEYLSYKIGFE-IVKTKNLLAFCTLPYRVLVKVI FLHRINILYKIKLKFNL

Query: 373 PPLETYPDYNEALKEKECFTYKLGEEFIK 401
P L+ Y DY++ K K Y+LG F+K
Sbjct: 664 PKLKDYVDYDDIFKIKNHLAYRLGSVFLK 692

tr Q9CMP1 HyaE (FcbE) [hyaE] [Pasteurella multocida] 6:
Q9CMP1_PASMU a:

Score = 62.8 bits (151), Expect = 2e-08

Identities = 56/200 (28%), Positives = 96/200 (48%), Gaps = 18/200

Query: 207 DIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTLENKHNNNSINDILLTD
+IEALK+ I+ NI D + F + E K + +L T+
Sbjct: 419 EIEALKI---IFNENISVQED---MQEKFQEANKRKQELEQELKAISDKKALLETE

Query: 267 VSFYKNQLKADNKIMLNFYNIHLSKDTLIKFLNKEIAVLK-KQTTQRAKARIQNHL
++ L+ +NK++L ++ + ++ L + VLK K A RI+N L
Sbjct: 473 TQVSES-LENENKVLLAQLQLIQEE---LEKLYIDNQVLKAKPRLYGAADRIKNQL

Query: 326 GQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY
G + + +S+ G + LPFI+ + K+E K Y++ LPP+ Y D
Sbjct: 529 GYKIQRHGRSLFGLIFLPFILFFTYLGFKREMKKYEWN-----TLPPIHEYEDA

Query: 386 KEKECFTYKLGEEFIKAGKN 405
+ K +YKLG F++ N
Sbjct: 582 RIKSHLSYKLGVLFLQEINN 601

tr Q4HGT1 Bifunctional alpha-2,3/-2,8-sialyltransferase [CCO1215] 44 AA
Q4HGT1_CAMCO [Campylobacter coli RM2228]
align

Score = 62.8 bits (151), Expect = 2e-08
Identities = 24/44 (54%), Positives = 35/44 (79%)

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYYLGKK 59
M+ I+ NGPS++ I+Y LP++YDVFRCN+FY E +Y++GKK
Sbjct: 1 MKAAIVTSNGPSMREIDYSLLPKDYDVFRCNFEFYHEREYFIGKK 44

tr O85456 HyaE [hyaE] [Pasteurella multocida] 62
O85456_PASMU al

Score = 62.8 bits (151), Expect = 2e-08
Identities = 56/200 (28%), Positives = 96/200 (48%), Gaps = 18/200

Query: 207 DIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTLENKHNNNSINDILLTD
+IEALK+ I+ NI D + F + E K + +L T+
Sbjct: 419 EIEALKI---IFNENISVQED---MQEKFQETNKRKQELEQELKAISDKKALLETE

Query: 267 VSFYKNQLKADNKIMLNFYNIHLSKDTLIKFLNKEIAVLK-KQTTQRAKARIQNHL
++ L+ +NK++L ++ + ++ L + VLK K A RI+N L
Sbjct: 473 TQVSES-LENENKVLLAQLQLIQEE---LEKLYIDNQVLKAKPRLYGAADRIKNQL

Query: 326 GQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY
 G + + +S+ G + LPFI+ + K+E K Y++ LPP+ Y D
 Sbjct: 529 GYKIQRHGRSLFGLIFLPFILFFTYLGFKREMKKYEWN-----TLPPIHEYEDA

Query: 386 KEKECFTYKLGEEFIKAGKN 405
 + K +YKLG F++ N
 Sbjct: 582 RIKSHLSYKLGVLFLQEINN 601

tr Q4HS04 Hypothetical protein [CUP1761] [Campylobacter
 Q4HS04_CAMUP upsaliensis RM3195]

Score = 61.6 bits (148), Expect = 4e-08
 Identities = 44/142 (30%), Positives = 67/142 (46%), Gaps = 30/142

Query: 288 LHSKDTL--IKFLNKEIAVLKKQTTQRAKAR-----IQNHLSYKLGQ
 L SK+ L +K N E+ + KKQ + R ++ HLSYKLGQ
 Sbjct: 243 LGSKENLKSLKAKNLELKIKKKQIVLKEFMRPKFILAQNESACFAVKQHLSYKLGQ

Query: 332 NSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKE
 SKS+ G++ LP+++ I +HK+E L + + DY EA
 Sbjct: 303 CSKSLFGYVCLPYVLYYIKSTHKKEN-----LETTQQFLDYEEAQNI

Query: 392 TYKLGEEFIKAGKNWYGEgyik 413
 +YKLG+ ++ + G Y K
 Sbjct: 349 SYKLGQGLLQRTRGGGGGNYAK 370

tr Q9AHN3 DcbE [dcbE] [Pasteurella multocida] 60
 Q9AHN3_PASMU al

Score = 57.8 bits (138), Expect = 6e-07
 Identities = 45/148 (30%), Positives = 73/148 (48%), Gaps = 22/148

Query: 258 ILLTDNTPGVSFYKNQLKADNKIMLNfynilHskDTLIKFLNKEIAVLKKQTTQRA
 I++ DN +NQ++A L F L K+ + +K A
 Sbjct: 457 IIIEDNIKEKKSLENQVEA-----LQF-----ELEKYFIENKKIKEKPPLWGA

Query: 318 QNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALP
 ++ L Y+LG+ +I S+S++GF+ LP ++ +S K + ++K+ N+
 Sbjct: 504 RSTLEYQLGRTMIEKRSRIIGFIMLPISLILGYLSFKISE-----IRKDKNII--

Query: 378 YPDYNEALKEKECFTYKLGEEFIKAGKN 405
 Y DY EA+K K +YKLGE FI KN
 Sbjct: 555 YQDY YEAMKLKNHLSYKLG EVFIINFKN 582

Score = 39.3 bits (90), Expect = 0.24
Identities = 16/41 (39%), Positives = 29/41 (70%)

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQE 356
+++NHLASYKLG+ IIN K+ + ++ LP+ + V + K++
Sbjct: 563 KLKNHLASYKLGEVFIINFKNPIKWILLPYRLYKTVFNFKKK 603

tr Q8L0V3 Hypothetical protein kfoB [kfoB] [Escherichia coli] 5
Q8L0V3_ECOLI 2

Score = 57.4 bits (137), Expect = 8e-07
Identities = 40/156 (25%), Positives = 77/156 (48%), Gaps = 10/156

Query: 273 QLKADNKIMLNFYNIHLSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQA
+L + +++LN +++ K N+ + + A RI + Y+LG
Sbjct: 387 KLSCEKELLNQLHLVQQKLEQYFIDNQRLEKKQLPELYGAAERITQDIGYRLGAV

Query: 333 SKSVLGFLSLPFIILSIVISHKQEQAQKAYKFKVKKNPNLALPPLETYPDYNEALKEK
SK+ LG +S+PF ++S E + +K K ++LP + Y D +EA + K
Sbjct: 447 SKTFLGLISIPFALIS-----EWRTWKKKYDSEYQVSLPSIFLYADKHEAERVK

Query: 393 YKLGEFEFIKAGKNWYGEYIKFIFKDVPRCLKREFEK 428
Y+LG+ I +N + G I F + R R+F++
Sbjct: 500 YQLGKLII--NQNHFPGLISLPF-SIYRTIRQFKR 532

Score = 36.2 bits (82), Expect = 2.0
Identities = 18/50 (36%), Positives = 29/50 (58%)

Query: 316 RIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQAQKAYKFKVK 365
R++ HLSY+LG+ +I + LG +SLPF I + K+ + + VK
Sbjct: 493 RVKKHLSYQLGKLIINQNHFPGLISLPFSIYRTIRQFKRTKNNSQVGVK 542

tr Q6EBB2 Tgh012 (Fragment) [Campylobacter jejuni] 4
Q6EBB2_CAMJE a

Score = 54.7 bits (130), Expect = 5e-06
Identities = 48/220 (21%), Positives = 101/220 (45%), Gaps = 22/22

Query: 213 LLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVS
+L + Y + LCD+S+ N+ ++ + + + N + +S

Sbjct: 259 ILNNRYDCFLKTLCDNSL-----NVFCDYYKKYLNQSKNNFFYIKFVAAYIS

Query: 273 QLKADNKIMLNFYNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQA
 + + + ++ H+ L+K ++K +K + R++ L YKLGQ

Sbjct: 310 DVYCALQYLDELISMKHNNNTLLKLIDK----IKYNLCYNGELRLKGTLOQYKLGQV

Query: 332 NSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKE
 +KS + +L + +K+E+K + ++ N N+ +P E DY+ A +

Sbjct: 366 FTKSNI-----IDVLFFLSRYKKEKKKIELFIQ-NFNINIPSFEQCYDYSNAKRI

Query: 392 TYKLGEFIKAGKNWYGEgyIKFIFKDVPRLLK-EFEKGE 430
 +Y +G+ I+A ++WY Y +K K +++KG+

Sbjct: 419 SYNIGKIMIQAHSWYKGAYFILPYKIYMLYKNFKYKKGK 458

tr Q4HTC3 Capsular polysaccharide biosynthesis protein,
 Q4HTC3_CAMUP putative [CUP0758]
 [Campylobacter upsaliensis RM3195]

Score = 54.7 bits (130), Expect = 5e-06
 Identities = 44/116 (37%), Positives = 60/116 (50%), Gaps = 8/116

Query: 313 AKARIQNHLASYKLGQALI-INSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKN
 A RI+NHLASYKLGQ LI N+ G +SL F + I +H + + K

Sbjct: 8 ATQRIKNHLASYKLGQELIKYNTGGGGGVISLLFKLYHIKKTTHKLTQFRKTLELAR

Query: 372 LPPLETYPDYNEALKEKECFTYKLGEFIKAGKNWYGEgyIKFIFKDVPRLLKREFE
 PPL D+NEAL K +Y+LG+ I K Y Y K + + K+EF+

Sbjct: 68 YPPLRQCDFDNEALWVKTHLSYRLGK--ILLKASYFNLYDK-----IKQAKKEFK

tr Q6KCZ4 KfiB protein [kfiB] [Escherichia coli] 56
 Q6KCZ4_ECOLI al

Score = 52.8 bits (125), Expect = 2e-05
 Identities = 33/119 (27%), Positives = 60/119 (49%), Gaps = 11/119

Query: 299 NKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFLSLPFIILSIVISHK
 N+EI A +I+ L Y+LG ++ SKS+ G +++PF ++ + K

Sbjct: 440 NQEIKKKLPPVLYGAAEQIKQELGYRLGYIIVSYSKSLKGIITMPFALIRECVFEK

Query: 359 AYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEFIKAGKNWYGEgyIKF
 +Y V PL Y D ++A + K+ +Y+LG+ I + + + G+I

Sbjct: 500 SYGVDV-----PLYLYADADKAERVKKHLSYQLGQAISSANSIF--GFITL

Score = 45.8 bits (107), Expect = 0.003
Identities = 17/40 (42%), Positives = 32/40 (79%)

Query: 316 RIQNHLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQ 355
R++ HLSY+LGQA+I ++ S+ GF++LPF ++ +V +++
Sbjct: 518 RVKKHLSYQLGQAISSANSIFGFITLPFKLIVVVYKYRR 557

tr Q43KB3 Similar to Chromosome segregation ATPases
Q43KB3_9CHLB [Cpha266DRAFT_2744]
[Chlorobium phaeobacteroides DSM 266]

Score = 50.4 bits (119), Expect = 1e-04
Identities = 33/134 (24%), Positives = 65/134 (47%), Gaps = 7/134

Query: 275 KADNKIMLNFNILHSDKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLSYKLGQALI
K +N+++L + + + N+++ + A RI++ L Y+LG +I
Sbjct: 534 KVENELLTQLHQVQEELERYYHENRKLKESQVPIYTGAPERIKHELPYRLGAVMI

Query: 335 SVLGFLSLPFIILSIVISHKQEQKAYKFKVKKPNLALPPLETYPDYNEALKEKEC
+ G+ +P + +E+KA+ + + LPPL Y D +A K K+
Sbjct: 594 TFSGWFIQIPAAALA-----REKKAFLKEKADQSHQTLPLILYRDVEQAKKIKKH

Query: 395 LGEEFIKAGKNWYG 408
LG ++ K+ G
Sbjct: 647 LGSILVEKNKSPIG 660

Score = 35.4 bits (80), Expect = 3.4
Identities = 15/42 (35%), Positives = 29/42 (68%)

Query: 316 RIQNHLSYKLGQALIINSSKSVLGFLSLPFIILSIVISHKQEQ 357
+I+ HLSY+LG L+ +KS +G+L +P+ + V + ++E+
Sbjct: 638 KIKKHLSYRLGSILVEKNKSPIGWLLMPYQLGREVFTFRKEK 679

tr Q6EBB6 Tgh006 (Fragment) [Campylobacter jejuni] 5:
Q6EBB6_CAMJE a.

Score = 48.5 bits (114), Expect = 4e-04
Identities = 37/140 (26%), Positives = 66/140 (46%), Gaps = 27/140

Query: 270 YKNQLKADNKIMLN---FYNILHSDKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLS
YKN K N + ++ F++ KD + N + ++K NHLS

Sbjct: 466 YKNYQKYFNDLEVDTCFFSCYQKKDLIS---NSAVLIVK-----NHLS
Query: 327 QALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYN
+ +++ K++ F+ +P II + K E+ +K L +E DYN
Sbjct: 511 K-ILLECKNLKDFVEIPIIIKYFLWESKNEKAYFKS-----FLFEIEKLDDYN
Query: 387 EKECFTYKLGEFIKAGKNW 406
+ +Y+LG+ I++ K W
Sbjct: 562 IRNYLSYQLGKLIIESFKGW 581

tr Q6EB08 Tgh120 (Fragment) [Campylobacter jejuni] 2
Q6EB08_CAMJE a.

Score = 48.1 bits (113), Expect = 5e-04
Identities = 27/71 (38%), Positives = 40/71 (56%), Gaps = 3/71 (4%)

Query: 358 KAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEFIKAGKNWY-GEGYI
K Y+ ++ P L P LET DY +AL+ K +Y LGE IKA K W+ G G+
Sbjct: 1 KIYQQTIQIFPQLKYP SLET CGDYE QALRYKFHLSYMLGEVLIKADKTWHKGS GF-
Query: 417 KDVPRLKREFE 427
D+ + +EF+
Sbjct: 59 NDIKKANKEFQ 69

tr Q8IBW2 Hypothetical protein MAL7P1.65 [MAL7P1.65]
Q8IBW2_PLAF7 [Plasmodium falciparum
(isolate 3D7)]

Score = 47.0 bits (110), Expect = 0.001
Identities = 58/266 (21%), Positives = 106/266 (39%), Gaps = 49/26

Query: 69 VFLQQYHTAKQLILKNEYEIK-----NIFCSTFNLPFIESNDFLH---QFYN
+F+ YH K I KN+ + N+ N+ E N + FYN
Sbjct: 493 IFINIYHINKTEINKNKC NVSKVNI SN SHNLINKDENVKLNEMNHNIS CN DHFYN
Query: 117 -----AKLGYEV IENLKEFYAYIKYNEIYFN-KRITSGVYMCAIAIALGY
K+ YE+I+++ F+ +K+ YF +IT+
Sbjct: 553 YIHL SKKYKNCIKINYEI IKS IHLFHL LKH FYNYFPILKITNN-----
Query: 165 LCGIDFYEGDVIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKV
L ++Y+ IYP+E + N + + +++ +KE I + K+ V
Sbjct: 601 LIIYNY YDKSYIYPYENNNNNKQNVIKNVENQTIDVLKNKEEKINNFNVFKN---V

Query: 225 LCDDSI LANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYK-----N
L D N N + +E+ + +DILL++N +S Y +
Sbjct: 658 L--DFFYFNETKNDENGTIHSLVESTKMENFDDILLSENEKELSSYNLPQNHISHD

Query: 277 DNKIMLNFYNI LHSKDTLIKFLNKEI 302
+ K N N L S+ + +N ++
Sbjct: 716 EEKDQHNSVNFLSSEKLFYLYLINNKL 741

tr Q4Y918 Hypothetical protein (Fragment) [PC000047.00.0]
Q4Y918_PLACH [Plasmodium
chabaudi]

Score = 46.6 bits (109), Expect = 0.001
Identities = 64/252 (25%), Positives = 108/252 (42%), Gaps = 54/25

Query: 59 KIKAVFFNPG---VFLQQYHTAKQLILKNEYEIKNIFCSTFNL-----PFIE
K+K + F G + + +++ ++ + KN+F S FNL P +E
Sbjct: 262 KLKNLIFENGNKQIDINKFNYTQERFINT---FKNVFDSIFNLIKLYYEIIPNLE

Query: 107 -LHQFYNFPPDAKLGYEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYK
LH N D + + N+ +F+ I Y+E + + +Y I + L +
Sbjct: 319 ILHFVCNHINDKNEYFTSLINIFKFFENIYSE-----HLENNIYFSLIRVCLNF-

Query: 166 CGIDFYEGDVIIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYD----IEALKLLKSI
FYE +V P + S +KT+ PSN H E +E + +KS
Sbjct: 372 ----FYEENVGDPPQLASALVKTLLE-----DPSNKHGVEVKLEVVELINFMKSK

Query: 220 VNIYALCDDSI LANH-----FPLSININNNFTLENKHNNNSINDILLTDNTPGVSFY
VNI ++ +L + PLS N NN + ++ +N + + F
Sbjct: 423 VNI----EERVLLIYTEYISISIPLENNLNNNSKKSSDNLVQSFY---TALYIDFS

Query: 275 KADNKIMLNFYN 286
N NFYN
Sbjct: 476 LFGN----NFYN 483

tr Q4HTQ9 Hypothetical protein [CUP0614] [Campylobacter
Q4HTQ9_CAMUP upsaliensis RM3195]

Score = 45.8 bits (107), Expect = 0.003
Identities = 40/137 (29%), Positives = 62/137 (45%), Gaps = 10/137

Query: 279 KIMLNFYNI LHSKDTLIKFLNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSK
KI L N + +D ++ N + + K +T A + I++HLSY++G+ +

Sbjct: 201 KIFLIPINYILHRDFFLQRENFRLGWVDKSTLTAVSVIKSHLSYQIGEIAM----
Query: 339 FLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYK
F F+I ++ I K KF ++ N L DY E +K K TYK
Sbjct: 257 FKERFFLIFTLAIKK-----KFNNQEKINSNYLYLSLCKDYPEFIKIKNSPTYK
Query: 399 FIKAGKNWYGEgyIKFI 415
I+ K G I FI
Sbjct: 311 IIEIHKKGGNLGLIHFI 327

tr Q9EMR1 AMV138 [AMV138] [Amsacta moorei entomopoxvirus
Q9EMR1_AMEPV (AmEPV)]

Score = 45.4 bits (106), Expect = 0.003

Identities = 56/191 (29%), Positives = 82/191 (42%), Gaps = 34/191

Query: 199 SNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFPLSININNFTLENKHNNNS
SNC S DI KL + N L DDS+ N +SI +N + +K ++
Sbjct: 61 SNCSSINNDIGISKLYEEECMEN-NILIDDSVNNNEIKISIEDHN--IIPSKKSS-

Query: 259 LLTDNTPGVSFYKNQLKADNKIMLNFYNILH-----SKDTLIKFLNKEIAVL
TD P ++ +N N+ + N N++ SK +IK LN E + L
Sbjct: 113 YFTDYMPEINIENNNV--NEKLKNVINVIEPNQDTIKDLSKTEIIKKLNNENSEL

Query: 310 TQRAKARIQNHLsyKLGQA-----LIINSKSVLGFLSLPFIILSIVISHKQE
K+ N L KL +IIN LG +SLP I I + K+
Sbjct: 171 KSMEKSENLNELMKKLNMCGNELINKKYVIINYAKTLG-ISLPLIDFEI-LDIKEI

Query: 361 ----KFKVKKN 367
K+KKN
Sbjct: 229 DIETIKIKKN 239

tr Q7RS84 TERT (Fragment) [PY00479] [Plasmodium yoelii 2:
Q7RS84_PLAYO yoelii] a.

Score = 45.4 bits (106), Expect = 0.003

Identities = 60/242 (24%), Positives = 96/242 (38%), Gaps = 53/242

Query: 193 IKDFKPSNCHS--KEYDIEA----LKLLKSIYKVNIYALCDDASILANHFPLSININ
IK+ KP H K+ DIE LKLLK K
Sbjct: 720 IKESKPKKVHMLKKQDIEQHLNQLKLLKKKKK-----

Query: 247 LENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHskDTLIKFLNKEI

```

      L +K NNSIN +   +N      K   K   N      F + +   K +I + KEI
Sbjct: 754 LLSKRNNNSINVVKSIEN-----KETGKDKNTKNTLFDKDKIIKKGNI--MCKEI

Query: 307 KQTTQRAKARIQNHLASYKLQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKF
      K+  +R      +   YK+      ++N K+V  +L   +   +      K+      K+
Sbjct: 805 KEKKKRLSECKKIDNLYKIK---VLNKKNVRPYLKKFYKYI-----RKKYFSLKKY

Query: 367 NPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPRL
      N N+      L   Y +Y   + +K+      +G+ F K   K      YIK  +K V ++
Sbjct: 857 NKNITPTMLRNYKEYINYMNDKKFLFIYMGRFFFKKK---VNYIKLFYKLVTKI

Query: 427 EK 428
      K
Sbjct: 913 NK 914

```

```

tr      Q8I474                      Hypothetical protein PFE0130c [PFE0130c] [Plasmodium
      Q8I474_PLAF7                  falciparum
                                      (isolate 3D7)]

```

Score = 45.4 bits (106), Expect = 0.003

Identities = 44/202 (21%), Positives = 75/202 (36%), Gaps = 51/202

```

Query: 170 FYEGDVIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYA
      +++ D+I+      ++ IF   + +      + + YD E   L KSIY +N+
Sbjct: 858 YHKKDIIIFHTHMFELFVRLIFENSRTYFTIFINEQTYDNE---LYKSIYYLNLCK

Query: 230 ILANHFPLSI-----NINNNFT
      I      + +      N NNN
Sbjct: 915 IYLGRTMMVTRVQNSIKNTSKNRKNNKNENNDKDDNNNNNNNNNNNNNNNNNNNN

Query: 252 NNSINDILLTDNTPGV-----SFYKNQLKADNKIMLNFYNILHSDTLIKFL
      NN  N+IL+ +   V      YKN+++  +KI+LN  N +  K+  ++ L
Sbjct: 975 NNKNNNILMCEEPNDVIDKLLRQNDIYKNEIQEKDKILLNLQNDIQKKNKTLEEL

Query: 304 VLKKQTTQRAKARIQNHLASYKL 325
      K      K   I   L YK+
Sbjct: 1035 KYKNDNLDNMK--IIQSLKYKI 1054

```

```

tr      Q8I3Z1                      Hypothetical protein PFE0570w [PFE0570w] [Plasmodium
      Q8I3Z1_PLAF7                  falciparum
                                      (isolate 3D7)]

```

Score = 43.5 bits (101), Expect = 0.013

Identities = 55/221 (24%), Positives = 93/221 (41%), Gaps = 32/221

```

Query: 122  EVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
           E+ E  K F  +IK   IYF KRI    ++                ++ Y+ +
Sbjct: 4673 EIYEIGKVFDHFIKNEIYFKKRINMLDFV-----MNDYKKENF

Query: 182  MSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP
           N K IF    ++   N ++K  D+ ++  L++IYK N +    + +   +
Sbjct: 4717 SDINNK-IFYVAYNYPININNNKNDLFSI-YLRTIYKCNEHFRNLNHVFFIYSN

Query: 242  NNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADN-KIMLNFYNILHSKDTLI
           +N F    NK N+  N                S +K + K D  K M NFY  +  K+
Sbjct: 4775 HNLFLFFNKDNDLFN-----SLFKLRFKIDQAKQMDNFYDYMEDKNN-N

Query: 301  EIAVLKKQTTQRAKARIQNHL-SYKLGQALIINSKSVLGFL 340
           E    +KK+                N + +YK  +  I NSKS + ++
Sbjct: 4823 EYVQIKKKNEENENITFSNPIGNKYKNY EYAIHNSKSDIFYI 4863

```

```

tr  Q55FU8      Hypothetical protein [DDB0189664] [Dictyostelium discoideum
    Q55FU8_DICDI (Slime
                  mold)]

```

Score = 43.5 bits (101), Expect = 0.013

Identities = 50/184 (27%), Positives = 74/184 (40%), Gaps = 27/184

```

Query: 229  SILANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYKNQL-----KADNK
           S L N + ++IN  NN    N +NN  ND    N P + + K  L    K++N
Sbjct: 319  SNLTNIYSITINNTNNSNNSNTNNN--NDDYF--NNPELLYSKLYLINLYVKSSENS

Query: 284  FYNILHSKDTLIKFLNKEIAVLKKQTTQRAKA-----RIQNHL-----
           FYN + S  TLI  N  +  K    +                +  NH++
Sbjct: 375  FYNRVKSSLTLIDLNNNMEDYKISFKMKIPEYAHLEVELYSFYQDPNHITPTITEG

Query: 327  QALIINSKSVLG-FLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY
           +  II    + G FL  FII  ++   K +++   K + N NL +    +  D
Sbjct: 435  KLFIIIFYPIFGAFLISTFIICLVLAIKKTKRRILMKQEPNVNLKIVKTQAKEDE

Query: 386  KEKE 389
           KEKE
Sbjct: 495  KEKE 498

```

```

tr  Q7RCB6      Hypothetical protein [PY05868] [Plasmodium yoelii 1
    Q7RCB6_PLAYO yoelii] a

```

Score = 42.4 bits (98), Expect = 0.028

Identities = 91/398 (22%), Positives = 157/398 (38%), Gaps = 70/39

```

Query: 34  KRLPREYDVFRN-QQFYFEDKYYLGKKIKAVFFNPGVFLQQYHTA---KQLILKNE
          KR+ + YD      N   F  K+++ K    V  N  G  F  Q+ ++      ++L N
Sbjct: 48  KRRIQIYDFPNTLNDIIFYKKFFINKLYNQVKQNKGNFDQENYSKIIYNNILLDN-

Query: 90  NIFCSTFNLFP-IESNDFLHQFYNFPPDAKLGYEVIENLKEFYAYIKYNEI----Y
          +  C   N+   I +  FL +FY F  +  + Y  + N+  +      KYN+I   +
Sbjct: 105 HTLCLYINIDKNILNFYFLSEFYKFLINKHINYRTLINMLIYDTNNKYNKINIFLF

Query: 145 ITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFPGIKDFKPSN
          I   +   A+ I+   K           D   +V   +       N  K     I +F   N
Sbjct: 165 ILKNILNYALLISGDKK-----DGNNNNVGLVYFLKKENDKFSKLNINEF---N

Query: 205 EYDIEALKLLKSIYKVNIALCDDSI LANHFPLSININNNFTLENKHNNNSINDILL
          DI   +  LK+   N++       IL N   +++N NN+  +       N ++ +IL+
Sbjct: 215 --DINNIASLKA---ENLFV-----ILKNIDFVNLNDNNSNSKGFMFNKNVINILM

Query: 265 PGVSFYKNQLKADNKIMLNFNILHSDTLIKFLNKEIAVLKKQTTQRAKARIQNH
          K  L  +N +H  +               LK++  +  K  I  N
Sbjct: 265 -----KEGLGLFNSIHKTN-----LKEKKNEETKKMIYN-

Query: 325 LGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPD
          L + +II  KS+  F +   ILSI   K  +K      +K  ++      T  +
Sbjct: 295 LKKEIIIIIFKSIYNFSN---SILSIFNLAKSGEKCVCINEKKQHIL-----TTCN

Query: 385 LKEKECFTYKLGEEFIKAGKNWYGEgyIKFIFKDVPR 422
          +K K           ++   K W G+   +  K+  +L
Sbjct: 347 IKHKNKNSDTKFFVYLSFRKEWGGKKKHfyFIKNCIKL 384

```

```

tr      Q8ILS2                      Hypothetical protein [PF14_0172] [Plasmodium
      Q8ILS2_PLAF7                  falciparum (isolate
                                   3D7)]

```

Score = 42.4 bits (98), Expect = 0.028

Identities = 35/138 (25%), Positives = 61/138 (43%), Gaps = 14/138

```

Query: 160 YKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFPGI--KDFKPSNCHSKEYDIEALKL
          +K+I  C +  +  D++       ++ NIK   PGI  K  K       E  ++  L
Sbjct: 276 FKSICTCSMLLH--DIL---NILNQNIKYDEPGIFQKSLKNIKIEKDELIMQNKL

Query: 218 YKVNIALCDDSI LANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYKNQ
          ++  + L D  ++   P+  NINNNF L++K+       L  N   +S Y+N
Sbjct: 331 LQIETFILRDPFLVEKLCPIHENINNNFLLKDKNK-----LYQNNKNISLYRNL

```

Query: 278 NKIMLNFYNILHSKDTLI 295
 NK + H K ++
Sbjct: 384 NKNFNLRKELFHYKQKIL 401

tr Q4YMV9 Hypothetical protein (Fragment) [PB001093.03.0] :
Q4YMV9_PLABE [Plasmodium berghei] :

Score = 42.4 bits (98), Expect = 0.028
Identities = 36/149 (24%), Positives = 66/149 (44%), Gaps = 21/149

Query: 289 HSKDTLIK-----FLNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSKS
 H+KDTL K + KE+ +KK+ +R + + YK+ ++N K+
Sbjct: 316 HTKDTLFDKDKIIKKGSTIMCKEVGKVKKEKKERMPECKKINNLYKIK---VLNKK

Query: 340 LSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKL
 L + + K+ K+ +K N N+ L Y +Y +K+ +
Sbjct: 373 LKKFYYKI-----RKKYFSLKKYYIKTNKNMIPMLRKYKEYINYTNDKKFLLIYM

Query: 400 IKAGKNWYGEgyIKFIFKDVPRLKREFEK 428
 K K YIK +K V +++++ K
Sbjct: 428 FKKKK---VNYIKLFYKLVIKIEKKINK 452

tr Q6EF78 Putative glycosyltransferase (Putative sugar transferase)
Q6EF78_CAMJE [HS23.18]
 [Campylobacter jejuni]

Score = 42.0 bits (97), Expect = 0.036
Identities = 36/129 (27%), Positives = 56/129 (42%), Gaps = 12/129

Query: 296 KFLNKEIAVLKKQTTQRAKARIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVI
 KFL + + K A I+ L Y++G+ L+ K +L ++ + I
Sbjct: 371 KFLLNKQSFafkyPLINASNIIFSLYRIGE-LLCKKKKILFIFNIIKALYDIKN

Query: 356 EQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEgy
 KF +K+ Y DY+EALK K +YKLG + + K WY
Sbjct: 430 ISHYKKFDLKE-----YIDYHEALKIKNHLSYKLGNAIVLSFKYWYKGRL

Query: 416 FKDVPRLLKR 424
 F+ V K+
Sbjct: 479 FELVSIYKK 487

Score = 38.9 bits (89), Expect = 0.31

Identities = 21/56 (37%), Positives = 33/56 (58%), Gaps = 2/56 (3%)

Query: 305 LKKQTTQRAKARIQNHLASYKLGQALIINSKSVLG--FLSLPFIILSIVISHKQEQK
LK+ +I+NHLSYKLG A++++ K L LPF ++SI HK+ ++
Sbjct: 438 LKEYIDYHEALKIKNHLSYKLGNAIVLSFKYWYKGRLLKLPFELVSIYKKHKRTRK

tr Q6EF55 Putative glycosyltransferase [Campylobacter jejuni]
Q6EF55_CAMJE

Score = 42.0 bits (97), Expect = 0.036

Identities = 36/129 (27%), Positives = 56/129 (42%), Gaps = 12/129

Query: 296 KFLNKEIAVLKKQTTQRAKARIQNHLASYKLGQALIINSKSVLGFSLPFIILSIVI
KFL + + K A I+ L Y++G+ L+ K +L ++ + I
Sbjct: 371 KFLLNKQSFAPKYPLINASNIKFSLEYRIGE-LLCKKKKILFIFNIIKALYDIKN

Query: 356 EQKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEY
KF +K+ Y DY+EALK K +YKLG + + K WY
Sbjct: 430 ISHYKKFDLKE-----YIDYHEALKIKNHLSYKLGNAIVLSFKYWYKGRLL

Query: 416 FKDVPRRLKR 424
F+ V K+
Sbjct: 479 FELVSIYKK 487

Score = 38.9 bits (89), Expect = 0.31

Identities = 21/56 (37%), Positives = 33/56 (58%), Gaps = 2/56 (3%)

Query: 305 LKKQTTQRAKARIQNHLASYKLGQALIINSKSVLG--FLSLPFIILSIVISHKQEQK
LK+ +I+NHLSYKLG A++++ K L LPF ++SI HK+ ++
Sbjct: 438 LKEYIDYHEALKIKNHLSYKLGNAIVLSFKYWYKGRLLKLPFELVSIYKKHKRTRK

tr Q98RL8 Hypothetical protein orf714 [orf714] [Guillardia theta
Q98RL8_GUITH (Cryptomonas
phi)]

Score = 41.2 bits (95), Expect = 0.062

Identities = 74/315 (23%), Positives = 124/315 (38%), Gaps = 61/31

Query: 10 LIVSKNMQNI IIIAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDKY YLGK-----
+ + KN+ NI N N K++ R + +F FE+ + + K

Sbjct: 79 ITILKNLNNIFFVNNW--FINAQNKILRSFLIFN---IIFENNFLICKTEMLNKY

Query: 59 -KIKAVFFNPGVFLQQYHTAKQ-----LILKNEYEIKNIFCSTFNLPFIESNDF
K+K +F F+ H +K L LK +IKN NL FI

Sbjct: 134 LKMKVIFIKKSFNLIHYSKIKNYNDSILKLKKNIKIKNFI----NLIFI-----

Query: 111 YNFFPDAKLGYEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTI-YL
YN Y ++ N K++ Y + +YF K I + + I + I Y

Sbjct: 182 YN-----YSIVSNFKKYEHYDFLSTLYFLKYIKFSLSIFTIVLKNIQSLIKYY

Query: 170 FYEGDVIYPFEAMST---NIKTIFPGIKD-FKPSNCHSKEYDIEALK----LLKSI
F + + + ++ ++IF +K+ FK S Y I +L L+K I

Sbjct: 234 FNRLFLFFIYIRINNNYQYQSIFNEMKNCFKNSIDFFIAYSIRSLNISRILIKRI

Query: 219 ---KVNIYALCDDASILANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVS--F
K N Y SI + F L+ + TL K L+ N+ + F

Sbjct: 294 LSIKCNFYIKNLLSINSKSFNLTSDSVKLITLNQKECKKYFLNLMQSNKLIETFF

Query: 274 LKADNKIMLNFYNIL 288
+K +NK++ +F N++

Sbjct: 354 MKNNNKVLYSFKNLI 368

tr Q7QPQ2 GLP_348_13351_18885 [Giardia lamblia ATCC 50803]
Q7QPQ2_GIALA

Score = 40.8 bits (94), Expect = 0.081

Identities = 43/168 (25%), Positives = 72/168 (42%), Gaps = 12/168

Query: 173 GDVIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCD
G +I P E + ++ F K F + K+ +++ALKL K I +LC+

Sbjct: 874 GVIIRPSEGLQAELQACFAESKAFNNLSADDKKVELKALKLRLQGMKSRISLCE

Query: 232 ANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYN
PL+ N+ +F+ ++ T N G SF+ + L D ++ N

Sbjct: 934 ITLPPLTDNMTGDFS-----RLTVPSTQATTNA-GTSFFHHTLHEDVSMGLGTQEN

Query: 289 HSKDTLIKFLNKEIAVLKKQTTQRAKA--RIQNHLSYKLGQALIINSK 334
S ++ + I+ L++ T+ A R LS KLG I K

Sbjct: 988 SSSKRIVSACERRISTLEQLNTELADRIYREVTRLSLKLGAIRFICCK 1035

tr P73984 Slr2117 protein [slr2117] [Synechocystis sp. (strain
P73984_SYNY3 PCC 6803)]

Score = 40.0 bits (92), Expect = 0.14

Identities = 40/158 (25%), Positives = 69/158 (43%), Gaps = 31/158

```
Query: 17 QNIIIAGNGPSLKNINIKRLPREYDVFRCNQFYFEDKYYLGKKIKAVFFNPGVFLQ
      ++ I GNGPSL ++ +L +Y F N+ Y +F + L
Sbjct: 38 EDCFIIGNGPSLKNKMDLAKL-NQYYTFGLNKIYL-----IFERVDSLSS

Query: 77 AKQLILKN-EYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEVIENLKEFY
      +L+++ + EI+N C F L F +S D + N + A G
Sbjct: 85 VNRLVIEQCQNEIQNFRPCPF-LEFTKSKDIIPFKENIYRLATTG-----R

Query: 136 YNEIYFNKRITSGVYMCAIAIAL----GYKTIYLCGID 169
      +I ++I G + +A+ L G+K ++L G+D
Sbjct: 134 QTDI--TQKICEGNTVTYVAMQLAYYMGFKRVFLIGVD 169
```

tr Q5M6S3 Putative sugar transferase [HS41.28] [Campylobacter
Q5M6S3_CAMJE jejuni]

Score = 40.0 bits (92), Expect = 0.14

Identities = 41/196 (20%), Positives = 89/196 (44%), Gaps = 17/196

```
Query: 216 SIYKVNIYALCDDSI LANHFPLSININNNFTLENKHNNNSINDILLTDNTPGVSFYK
      SI Y++ +S L + L I + N ++ S+N I V Y
Sbjct: 264 SISNQKQYSINTNSYL---YALYIEFDKNTYELKRYQMSMNWIFTCLELIKVLKYN

Query: 276 ADNKIMLNFYNILHSKDTLIKFLNKEIAVLKKQTTQ-----RAKARIQNHL
      + F L + +I F++K+ +LK + + ++ L
Sbjct: 321 ISILVEQTFLPTLLDRTLIIFFIDKDPLLLKNKLQELKDYFEKFHLSGAECKLYQL

Query: 326 GQALIINSKSVLGLSLPFIILSIVISHKQEQKAYKFKVKKNPNLALPPLETYPDY
      GQ ++ N +S+ G + + +++++ ++EQ+ ++ +K P + + +
Sbjct: 381 GQFVLSNYRSLRGLIKIVLNAKKMILNIQKEQELFQETIKNYPFIV---FSSSED

Query: 386 KEKECFTYKLGEEFIK 401
      K K+ ++Y+LG +F+K
Sbjct: 438 KIKKHYSYRLG-KFLK 452
```

tr Q8EWI3 Hypothetical protein MYPE2220 [MYPE2220]
Q8EWI3_MYCPE [Mycoplasma penetrans]

Score = 39.7 bits (91), Expect = 0.18

Identities = 40/152 (26%), Positives = 74/152 (48%), Gaps = 20/152

Query: 2 TRTRMENELIVSKNMQNIIIIAGNGPSLKNINIKRLPREYDVFRGNQFYFEDKYIYL
T ++N +++ N N ++ +LK ++ K L + +D N ++E KY+L
Sbjct: 484 TLEEIKNNILIKSNTLNSLLL---NLKELDIKYLEKNWD---NLSWYE-KYFLS

Query: 62 AVFFNPGVFLQQYHTAKQLI-LKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPD
VF VF+ + K+ L+N+ E++ IF F ++ N +++ F
Sbjct: 535 EVF---KVFVYDNYNKKRFFNLRNKNEVEQIFNKIFLNLYLSKN--VNKNIQFLKK

Query: 121 YE-VIEN---LKEFYAYIKYNEIYFNKRITSG 148
+ +IEN + Y YIK NE+Y + + +G
Sbjct: 590 IKYIIENKLVKNKSYFYIK-NEMYSSPNVLNG 620

tr Q8I232 Hypothetical protein PFA0550w [PFA0550w]
Q8I232_PLAF7 [Plasmodium falciparum
(isolate 3D7)]

Score = 39.7 bits (91), Expect = 0.18

Identities = 58/261 (22%), Positives = 99/261 (37%), Gaps = 32/261

Query: 56 LGKKIKAVFFNPGVFLQQ-----YHTAKQLILKNEYEIKNIFCSTFNLPFIESND
L KK K + + ++ Y+T + +KN IKN N E++
Sbjct: 166 LNKKNKTKSYTDNLLIENNNKKKNYNTKNNINIKNNINIKNKISKINIKTIEENSH

Query: 110 FYNFFPDAKLGYEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYL
+ D+ Y I+N++ Y KY N I + +Y I+ + YK L
Sbjct: 226 --RAYTDS---YYNIKNMRSNMYYSKY---MNTDINNLYKDKISSDIFYKDKIL

Query: 169 -----DFYEGDVIYPFEAMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLK-
+ Y + + N F K S+ K+ + + + +
Sbjct: 277 KKENMNCDNLYNNEKKTKKKTFLVNQAVFFTPKKSVLNSSNEKKDTEYKKSQNMND

Query: 217 IYKVNIYALCDDASILANHFPLSININNNFTLENKH-NNSINDILLTDNTPGVVSFYK
I +N ++L + + N IN NNN N + NN +N+I G +
Sbjct: 337 IDNMNNSLYNQTYETNSLKSIIINNNSNNNSNNNYLNNIEEKRKRNGTFIGIQ

Query: 276 ADNKIML---NFYNILHSDKT 293
++L N N+ +KDT
Sbjct: 397 RKENLLLDNKNINNVNITKDT 417

tr Q8IDZ6 Hypothetical protein PF13_0182 [PF13_0182]
Q8IDZ6_PLAF7 [Plasmodium falciparum
(isolate 3D7)]

Score = 39.7 bits (91), Expect = 0.18

Identities = 25/97 (25%), Positives = 48/97 (48%), Gaps = 4/97 (4%)

Query: 199 SNCHSKEYDIEALKLLKSIYKVNIYALCDDASILANHFPLSININNNFTLENKHNN
S + ++Y++ +LLK + + + H ++N+NNNFT N+ +
Sbjct: 1352 STSYEQKYNVHEKELLKDLNNTKKSDHKSELKKVLRHDISNVNVNNNFTESNRSCS

Query: 259 -LLTDNTPGVSFYKNQL---KADNKIMLNFYNNILHSK 291
+L + Y NQ+ DNK + F+N + K
Sbjct: 1412 EMLPYKKLNIYIYNNQIIVRNNDNKNLFYFFNANYEK 1448

Database: EXPASY/UniProtKB

Posted date: Dec 7, 2005 2:42 AM

Number of letters in database: 880,353,591

Number of sequences in database: 2,699,091

Lambda	K	H
0.322	0.141	0.412

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 430

length of database: 880,353,591

effective HSP length: 131

effective length of query: 299

effective length of database: 526,772,670

effective search space: 157505028330

effective search space used: 157505028330

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.9 bits)

S2: 76 (33.9 bits)

Wallclock time: 9 seconds



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CLUSTAL FORMAT for T-COFFEE Version 1.37, CPU=0.00 sec, SCORE=6300, Nseq=2, Len=434

```
unk|VIRT7553|Blast_submission      MTRTRMENELIVSKNMQNI IAGNGPSLKNINYKRLPREYDVFRCNQFYFEDK
tr|Q5DT12|Q5DT12_CAMJE             -----MKKVIIAGNGPSLKEIDYSRLPNDFDVFRCNQFYFEDK
                                     *.....*
                                     *** .....
```

```
unk|VIRT7553|Blast_submission      KAVFFNPGVFLLQYYHTAKQLILKNEYEIKNIFCSTFNLFPFIESNDFLHQFYNF
tr|Q5DT12|Q5DT12_CAMJE             KAVFYNPSSLFFEQQYYTLKHLIQNQEYETELIVCSNFNLTHIESENFLKNFYDY
****.*.:*:***** *:* :***** : * ** ***** :*****:*****:
```

```
unk|VIRT7553|Blast_submission      YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEG
tr|Q5DT12|Q5DT12_CAMJE             YDFFKQLKEFNAYFKFHEIYFNQRITSGIYMCABAIALGYKEIYLSGIDFYQN
*.:.:***** **.:.:*****:*****:*****:***** **.******:
```

```
unk|VIRT7553|Blast_submission    AMSTNIKTIFPGIKDFKPSNCH---SKEYDIEALKLLKLSIYKVNIYALCDDS
tr|Q5DT12|Q5DT12_CAMJE          TKQKNLLKL--VSNEFKNDNSHYIGHSKNTDLKALEFLEKTYKIKLYCLCPNS
.:*:.:.: :*** **      ***:*:~::~: ~::~::~:~:::
```

```
unk|VIRT7553|Blast_submission    LSININNNFTLENKHNNNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNIHL
tr|Q5DT12|Q5DT12_CAMJE          LAPNLNSNFIKKKKNNYTKDILIPSSSEAYGKFSKNIIFKKIKIKENIY---
*: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *: *
```

```
unk|VIRT7553|Blast_submission      FLNKEIAVLKKQTTQRAKARIQNHLASYKLGGQALIINSKSVLGFLSLPFIILSI
tr|Q5DT12|Q5DT12_CAMJE            -----
```

```
unk|VIRT7553|Blast_submission    QKAYKFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGE
tr|Q5DT12|Q5DT12_CAMJE          -----YKLIKDLLR-----
                                   ***  ....
```

```
unk|VIRT7553|Blast_submission      KDVPRCLKREFEKGGE
tr|Q5DT12|Q5DT12_CAMJE             --LPSDIKHIFYKGGK
                                     :*      :.: **:
```

- ☐ tr Q3B9W3 _NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9W2 _NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9V9 _NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9V8 _NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9V6 _NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ tr Q3B9V4 _NEIGO Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae]
- ☐ sp P72097 LST_NEIMB CMP-N-acetylneuraminate-beta-galactosamide-a.
- ☐ sp Q9JUV5 LST_NEIMA CMP-N-acetylneuraminate-beta-galactosamide-a.
- ☐ tr Q19993 _CAEEL Hypothetical protein [F34D10.3] [Caenorhabditis
- ☐ tr Q93S90 _XANCP Integral membrane protein WxcO [wxcO] [Xanthomon
- ☐ tr O16316 _CAEEL Hypothetical protein [C05C8.8] [Caenorhabditis e
- ☐ tr Q9XIR3 _ARATH F13011.12 protein [F13011.12] [Arabidopsis thali

Graphical overview of the alignments

[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

Matches on query sequence

Submission

LST_NEIGO

Q5F7T9

Q3B9W3

Q3B9W2

Q3B9V9

Q3B9V8

Q3B9V6

Q3B9V4

LST_NEIMB

LST_NEIMA

Q19993

Q93S90

O16316

Q9XIR3

Submission

Identity 0 25 50 75 100%

Alignments

sp P72074 CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 371 AA
 LST_NEIGO 3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside
 alpha-2,3-sialyltransferase) (Alpha 2,3-ST) align
 (Lipooligosaccharide sialyltransferase) [lst]

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKKVCLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr	Q5F7T9	Alpha-2,3-sialyltransferase [NGO1081] [Neisseria	378
	Q5F7T9_NEIG1	gonorrhoeae	AA
		(strain ATCC 700825 / FA 1090)]	align

Score = 77.8 bits (176), Expect = 3e-14
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKKVCLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

```
tr  Q3B9W3          Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA
    Q3B9W3_NEIGO
                                           align
```

Score = 77.8 bits (176), Expect = 3e-14
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKKVCLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

```
tr  Q3B9W2          Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA
    Q3B9W2_NEIGO
                                           align
```

Score = 77.8 bits (176), Expect = 3e-14
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKKVCLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr Q3B9V9 Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA
Q3B9V9_NEIGO
align

Score = 77.8 bits (176), Expect = 3e-14
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKKVCLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr Q3B9V8 Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA
Q3B9V8_NEIGO
align

Score = 77.8 bits (176), Expect = 3e-14
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKKVCLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr Q3B9V6 Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA
Q3B9V6_NEIGO
align

Score = 77.8 bits (176), Expect = 3e-14
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKKVCLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

tr Q3B9V4 Lst (EC 2.4.99.-) [lst] [Neisseria gonorrhoeae] 378 AA
Q3B9V4_NEIGO
align

Score = 77.8 bits (176), Expect = 3e-14
Identities = 22/22 (100%), Positives = 22/22 (100%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKKVCLTVLCLIVFCFGIFY

Sbjct: 1 MGLKKVCLTVLCLIVFCFGIFY 22

sp P72097 CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 371 AA
LST_NEIMB 3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside
alpha-2,3-sialyltransferase) (Alpha 2,3-ST) align
(Lipooligosaccharide sialyltransferase) [lst]
[Neisseria meningitidis serogroup B]

Score = 74.0 bits (167), Expect = 4e-13
Identities = 21/22 (95%), Positives = 21/22 (95%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKK CLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKA CLTVLCLIVFCFGIFY 22

sp Q9JUV5 CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 371 AA
LST_NEIMA 3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside
alpha-2,3-sialyltransferase) (Alpha 2,3-ST) align
(Lipooligosaccharide sialyltransferase) [lst]
[Neisseria meningitidis serogroup A]

Score = 74.0 bits (167), Expect = 4e-13
Identities = 21/22 (95%), Positives = 21/22 (95%)

Query: 1 MGLKKVCLTVLCLIVFCFGIFY 22
MGLKK CLTVLCLIVFCFGIFY
Sbjct: 1 MGLKKA CLTVLCLIVFCFGIFY 22

tr Q19993 Hypothetical protein [F34D10.3] 147 AA
Q19993_CAEL [Caenorhabditis elegans] align

Score = 32.9 bits (70), Expect = 0.97
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 6/18 (33%)

Query: 11 LCLIVF-----CFGI-FY 22
LCLIVF CFG+ FY
Sbjct: 39 LCLIVFATDAACFGVLFY 56

tr Q93S90 Integral membrane protein WxcO [wxcO] [Xanthomonas 750
Q93S90_XANCP campestris pv. AA

campestris]

align

Score = 31.6 bits (67), Expect = 2.3

Identities = 10/18 (55%), Positives = 14/18 (77%)

Query: 5 KVCLTVLCLIVFCFGIFY 22

K+ LTVL L+ CFG++Y

Sbjct: 199 KIALTVLYLVLSFCFVYY 216

tr 016316 Hypothetical protein [C05C8.8] [Caenorhabditis 387 AA
016316_CAEL elegans] align

Score = 31.2 bits (66), Expect = 3.1

Identities = 12/23 (52%), Positives = 15/23 (65%), Gaps = 7/23 (30)

Query: 4 KKVCLTVLCL--IVFCFG---IF 21

KK+ +LCL I+FCFG IF

Sbjct: 6 KKI--VILCLRLIIFCFGLGIIF 26

tr Q9XIR3 F13011.12 protein [F13011.12] [Arabidopsis thaliana 427
Q9XIR3_ARATH (Mouse-ear AA
cress)] align

Score = 30.3 bits (64), Expect = 5.6

Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 11 LCLIVFCFGI 20

LCL VFCF I

Sbjct: 116 LCLLVFCFSI 125

Database: EXPASY/UniProtKB

Posted date: Dec 7, 2005 2:42 AM

Number of letters in database: 880,353,591

Number of sequences in database: 2,699,091

Lambda	K	H
0.346	0.297	2.06

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
length of query: 22
length of database: 880,353,591
effective HSP length: 13
effective length of query: 9
effective length of database: 845,265,408
effective search space: 7607388672
effective search space used: 7607388672
T: 16
A: 40
X1: 15 (7.5 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 40 (21.7 bits)
S2: 63 (29.9 bits)

Wallclock time: 1 seconds

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